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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:18:06 ; Search time 270.325 Seconds
(without alignments)
425.847 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVQLQQSGAELVRPQTSV.....GSEQKLISEDLNSHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	100.0	262	4 AAB70762	Aab70762 Single ch
2	1122	80.4	264	7 ADE23202	Ade29202 Multivale
3	1002	71.8	248	2 AAW58826	Aaw58826 Human CD3
4	946.5	67.8	562	6 ABR57058	Abr57058 Plasmid p
5	942.5	67.6	594	9 ABE29087	Aeb29087 Immunokin
6	938	67.2	288	2 AAW82482	Aaw82482 Mouse bis
7	936	67.1	288	2 AAW82317	Aaw82317 Mouse bis
8	936	67.1	288	2 AAW82316	Aaw82316 Mouse OKT
9	930	66.7	539	3 AAY50823	Aay50823 Fv-antibo
10	930	66.7	554	3 AAY50822	Aay50822 Fv-antibo
11	919.5	65.9	269	8 ADR28054	Adr28054 NPB polyp
12	917.5	65.8	283	8 ADF85426	Adf85426 V122scFv
13	911.5	65.3	267	8 ADR70320	Adr70320 Polioviru
14	909.5	65.2	267	8 ADP84954	Adp84954 Single ch
15	906	64.9	264	8 ADP84957	Adp84957 Single ch
16	905.5	64.9	263	8 ADP84958	Adp84958 Single ch
17	905.5	64.9	562	6 ABR57059	Abr57059 Plasmid p
18	905	64.9	266	8 ADP84955	Adp84955 Single ch
19	904	64.8	262	8 ADP84959	Adp84959 Single ch
20	904	64.8	268	8 ADR70319	Adr70319 Polioviru
21	902.5	64.7	261	8 ADP84960	Adp84960 Single ch
22	902.5	64.7	265	8 ADP84956	Adp84956 Single ch
23	902	64.7	260	8 ADP84961	Adp84961 Single ch
24	901.5	64.6	259	8 ADP84962	Adp84962 Single ch

25	900	64.5	276	8 ADP84953	Adp84953 Single ch
26	900	64.5	294	9 ADZ66387	Adz66387 MOF11 ant
27	897	64.3	258	8 ADP84963	Adp84963 Single ch
28	895.5	64.2	240	6 ABJ26742	Abj26742 VEGF bind
29	895.5	64.2	240	8 ADK18245	Adk18245 Mouse VEG
30	895	64.2	268	8 ADR70385	Adr70385 Polioviru
31	895	64.2	268	8 ADR70386	Adr70386 Polioviru
32	892.5	64.0	257	8 ADP84964	Adp84964 Single ch
33	891.5	63.9	296	8 ADS20752	Ads20752 SBP tagge
34	876.5	62.8	241	2 AAW09435	Aaw09435 Anti-CD19
35	876.5	62.8	242	2 AAW09444	Aaw09444 Modified
36	875	62.7	500	9 ADV66137	Adv66137 Anti-CD3-
37	875	62.7	503	9 ADV66133	Adv66133 Anti-CD3-
38	875	62.7	503	9 ADV66135	Adv66135 Anti-CD3-
39	867.5	62.2	288	2 AAW82743	Aaw82743 Fusion pr
40	859.5	61.6	1033	9 AEB29091	Aeb29091 Immunokin
41	858	61.5	240	6 ABU07881	Abu07881 Venezuela
42	856.5	61.4	255	7 ADF72734	Adf72734 His-tagge
43	856	61.4	240	6 ABU07883	Abu07883 Venezuela
44	855	61.3	500	9 ADV66095	Adv66095 Anti-CD3-
45	855	61.3	503	9 ADV66087	Adv66087 Anti-CD3-

ALIGNMENTS

RESULT 1

AAB70762
ID AAB70762 standard; protein; 262 AA.

XX AC AAB70762;

DT 18-MAY-2001 (first entry)

DE Single chain Fv antibody construct anti-CD16 VH domain protein.

XX Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
KW tumor cell; natural killer cell activation; Hodgkin's disease;
KW Reed-Sternberg disease.

XX Synthetic.

XX DE19937264-A1.

XX 15-FEB-2001.

XX 06-AUG-1999; 99DE-01037264.

XX 06-AUG-1999; 99DE-01037264.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;

XX WPI; 2001-184000/19.

XX N-ESDB; AAF61152.

XX New Fv-antibody construct, useful for treating Hodgkin and Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30 surface protein.

XX Disclosure; Page 10; 18pp; German.

XX This invention describes a novel Fv-antibody construct (1) having binding sites for a CD16 receptor and a CD30 surface protein. The invention also describes (1) expression vector encoding (1); (2) transformants containing the vector of (1); (3) preparation of (1) by culturing cells of (2); and (4) a kit comprising (1) and/or the vector of (1), and CC auxiliaries such as buffers, solvents, carriers, controls and labels, or CC their replacements. The products of the invention have cytostatic activity. (1) causes lysis of CD30+, specifically tumor, cells. It CC activates natural killer cells, through the CD16 receptor, and directs CC them to CD30-expressing cells. (1) are used to treat diseases in which

CC CD30+ cells are implicated, particularly tumors and specifically Hodgkin
 CC or Reed-Sternberg diseases. (1) have a stronger lytic action than known
 CC bispecific antibodies, can be produced on a large scale with high purity,
 CC and contain no components that can induce unwanted immune responses
 XX
 SQ Sequence 262 AA;

Query Match 100.0%; Score 1395; DB 4; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.7e-94;
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQVQLQSGAEELVRPGTSVKISCKASGYTFNFWLQWVKQRPQGHLEWIGDIYPGGGYT 60
 DB 1 MAQVQLQSGAEELVRPGTSVKISCKASGYTFNFWLQWVKQRPQGHLEWIGDIYPGGGYT 60
 QY 61 NYNEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVTSSA 120
 DB 61 NYNEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVTSSA 120
 QY 121 KTPKLGDIELTQSPKFMSTSGDRVNTYKASQNVGTNVAWFQKPGQSPKVLIIYSAS 180
 DB 121 KTPKLGDIELTQSPKFMSTSGDRVNTYKASQNVGTNVAWFQKPGQSPKVLIIYSAS 180
 QY 181 YRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQVHTYPLTFGGGTGLEIKRADAA 240
 DB 181 YRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQVHTYPLTFGGGTGLEIKRADAA 240
 QY 241 AAGSEQKLISEEDLNHHHHH 262
 DB 241 AAGSEQKLISEEDLNHHHHH 262

RESULT 2

ADE29202
 ID ADE29202 standard; protein; 264 AA.

AC ADE29202;

XX 29-JAN-2004 (first entry)

XX Multivalent multimeric antibody CD19xCD16 related protein 2.

XX multivalent multimeric antibody; bispecific diabody; BsdB;
 KW human B cell marker; CD19; human Fc gamma receptor III; CD16; cytostatic;
 KW immunosuppressive; B-cell malignancy; non-Hodgkin lymphoma;
 KW B-cell mediated autoimmune disease; B-cell depletion; immune response;
 KW human anti-murine antibody response; CD19 x CD16 BsdB; PSKID19x16; mouse;
 KW murine.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Region 31..35
 FT /label= Complementarity_determining_region_H1
 FT Region 50..66
 FT /label= Complementarity_determining_region_H2
 FT Region 99..106
 FT /label= Complementarity_determining_region_H3
 FT Region 117..126
 FT /label= Synthetic_linker
 FT Region 130..164
 FT /label= Complementarity_determining_region_L1
 FT Region 180..186
 FT /label= Complementarity_determining_region_L2
 FT Region 219..225
 FT /label= Complementarity_determining_region_L3
 FT Region 247..257
 FT /label= c-myc_epitope
 FT Region 259..264
 FT /label= 6xHis_tag

XX EP1314741-A1.

XX

PD 28-MAY-2003.
 XX
 PF 14-NOV-2001; 2001EP-00127061.
 XX
 PR 14-NOV-2001; 2001EP-00127061.
 XX
 PA (AFFI-) AFFIMED THERAPEUTICS AG.
 XX
 XX Le Gall F, Kipriyanov MS, Moldenhauer G, Little M, Cochlovius B;
 PI Schaefer JH;
 XX
 DR WPI; 2003-620028/59.
 DR N-PSDB; ADE29201.
 XX
 PT Multivalent multimeric antibody for treating B-cell malignancies such as
 PT non-Hodgkin lymphoma, comprises specificities, and antigen-binding domain
 PT specific to human CD19 and CD16.
 XX
 PS Example 1; SEQ ID NO 2; 38pp; English.

XX This invention relates to a novel multivalent multimeric antibody (a
 CC bispecific diabody - BsdB) which comprises at least two binding sites
 CC specific for the human B cell marker CD19 and human Fc gamma receptor III
 CC (CD16). The invention may allow the development of compositions with
 CC cytostatic or immunosuppressive activity. The antibody is useful for the
 CC diagnosis and treatment of B-cell malignancies such as non-Hodgkin
 CC lymphoma, B-cell mediated autoimmune diseases or the depletion of B-
 CC cells. The multivalent multimeric antibody avoids the undesired immune
 CC response such as human anti-murine antibody response. The specification
 CC provides a process for stable high yield of recombinant antibodies. The
 CC present sequence is that of a mature mouse derived protein encoded by the
 CC DNA sequence of the CD19 x CD16 BsdB in the expression plasmid pSKID19x16
 CC which was used in the exemplification of the invention.

XX SQ Sequence 264 AA;

Query Match 80.4%; Score 1122; DB 7; Length 264;

Best Local Similarity 81.4%; Pred. No. 2e-74; Mismatches 14; Indels 4; Gaps 1;
 Matches 215; Conservative 14;

QY 3 QVQLQSGAEELVRPGTSVKISCKASGYTFNFWLQWVKQRPQGHLEWIGDIYPGGGYTNY 62
 DB 1 QVQLQSGAEELVRPGTSVKISCKASGYTFNFWLQWVKQRPQGHLEWIGDIYPGGGYTNY 60
 QY 63 NEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVTSSAKT 122
 DB 61 NEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVTSSAKT 120
 QY 123 TPKLGGDIELTQSPKFMSTSGDRVNTYKASQNV---GTNVAWFQKPGQSPKVLIIYS 178
 DB 121 TPKLGGDIILLTQTPASLAVSLGQRATISCKASQSDYDGDSDYLNWYQQLPGQPPKLLIYD 180
 QY 179 ASYRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQVHTYPLTFGGGTGLEIKRAD 238
 DB 181 ASNLVSGIIPRFSGSGSGTDFLTINHPVEKVDAAVTHCQSTEDPWTFTGGGTGLEIKRAD 240
 QY 239 AAAAGSEQKLISEEDLNHHHHH 262
 DB 241 AAAAGSEQKLISEEDLNHHHHH 264

RESULT 3

AAW58826
 ID AAW58826 standard; protein; 248 AA.

XX AAW58826;

XX 18-AUG-1998 (first entry)

XX Human CD30 binding protein.

KW CD30 binding protein; human; suppressor; proliferation; metastasis;
 KW tumour formation; CD30 antigen.

XX OS Homo sapiens.
 XX PN DE19640733-A1.
 XX PD 09-APR-1998.
 XX PF 02-OCT-1996; 96DE-01040733.
 XX PR 02-OCT-1996; 96DE-01040733.
 XX PA (ABKE/) ABKEN H.
 XX WI; 1998-218120/20.
 XX DR N-PSDB; AAV11399.
 XX PT Polypeptide than binds to CD30 without cell activation - for inhibiting
 PT proliferation and metastasis of tumour cells, etc.
 XX PS Claim 3; Page 7-8; 8pp; German.
 XX CC This sequence represents a human CD30 binding protein which can be used
 CC in a method for suppressing unchecked proliferation, tumour formation and
 CC metastasis of cells expressing the CD30 antigen. This protein
 CC specifically binds to CD30 without inducing cell activation by CD30. The
 CC protein can also be used for probing, binding or enriching CD30-
 CC expressing cells in vivo or in body fluids, cell suspensions or tissues
 CC in vitro. A substance coupled to the protein accumulates in the vicinity
 CC of CD30-expressing cells in vivo or in vitro
 XX SQ Sequence 248 AA;

Query Match 71.8%; Score 1002; DB 2; Length 248;
 Best Local Similarity 79.0%; Pred. No. 1.2e-65;
 Matches 196; Conservative 12; Mismatches 28; Indels 12; Gaps 2;
 QY 1 MAQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGVKORPGHLEWIGDIYPGGGYT 60
 DB 1 MAQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGVKORPGHLEWIGDIYPGGGYT 60
 QY 61 NYNEKFGKATVTADTSSRTAYVQVRLTSSEDSAVYFCARSASW-----YFDVWGARTT 114
 DB 61 DYNQNFQKGTTLTADKSNATYMQLSLTSSEDSAVYFCARSADYGVETWYFAYWGGTT 120
 QY 115 VTSSAKTTPKLG-----DIETQSPKFMSTSGDRVNVYTKASQNVGTVNVAWFOQKP 168
 DB 121 VTSSGG 180
 QY 169 GQSPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHTYPLTFGG 228
 DB 181 GQSPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHTYPLTFGG 240
 QY 229 GTKLEIKR 236
 DB 241 GTKLEIKR 248

RESULT 4
 ABR57058
 ID ABR57058 standard; protein; 562 AA.
 XX AC ABR57058;
 XX DT 05-AUG-2003 (first entry)
 XX DE Plasmid pSKK2 scfv3-LL-Db19 amino acid sequence.
 XX KW Multimeric single chain tandem Fv-antibody; antibacterial; virucide;
 KW cytostatic; cytokine antagonist; diagnosis; viral disease; prion disease;
 KW bacterial disease; tumoural disease; agglutination; red blood cell;
 KW immune system; tumour cell; cytokine; cytotoxic.
 XX OS Synthetic.

XX EP1293514-A1.
 XX 19-MAR-2003.
 XX 14-SEP-2001; 2001EP-00122104.
 XX 14-SEP-2001; 2001EP-00122104.
 XX (AFFI-) AFFIMED THERAPEUTICS AG.
 XX Le Gall F, Kipriyanov S, Reusch U, Moldenhauer G, Little M;
 XX WPI; 2003-395536/38.
 XX DR N-PSDB; ACC79606.
 XX PT New multimeric Fv-antibody having monomers forming antigen-binding units
 PT and sites, useful for the preparation of a pharmaceutical composition for
 PT the treatment of a viral, bacterial, tumoral or prion diseases.
 XX Example 1; Fig 6A-B; 29pp; English.
 XX CC The present invention describes a multimeric Fv-antibody (I) comprising:
 CC (a) monomers comprising at least 4 variable domains of which two
 CC neighbouring domains of one monomer form an antigen-binding VH-VL or VL-
 CC VH scFv unit; and/or (b) at least 2 variable domains of a monomer that
 CC are non-covalently bound to 2 variable domains of another monomer
 CC resulting in the formation of at least 2 additional antigen binding sites
 CC to form multimerisation motif. Also described is a process for the
 CC preparation of (I) comprising ligating DNA sequences encoding the peptide
 CC linkers with the DNA sequences encoding the variable domains such that
 CC the peptide linkers connect the variable domains of the multivalent
 CC multimeric Fv-antibody, and expressing the DNA sequences encoding the
 CC various monomers in an expression system. (I) has antibacterial, virucide
 CC and cytostatic activities, and can be used as a cytokine antagonist. The
 CC multimeric Fv-antibody is useful for diagnosis. The antibody can also be
 CC used for the preparation of a pharmaceutical composition for the
 CC treatment of a viral, bacterial, tumoural or prion disease, the
 CC agglutination of red blood cells, linking cytotoxic cells of the immune
 CC system to tumour cells, or linking activating cytokines, cytotoxic
 CC substances or a protease to a target cell. The present sequence
 CC represents the plasmid pSKK2 scfv3-LL-Db19 amino acid sequence, which is
 CC used in the exemplification of the present invention

XX SQ Sequence 562 AA;
 Query Match 67.8%; Score 946.5; DB 6; Length 562;
 Best Local Similarity 68.0%; Pred. No. 3.5e-61;
 Matches 185; Conservative 29; Mismatches 47; Indels 11; Gaps 3;
 QY 2 AQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGVKORPGHLEWIGDIYPGGGYT 61
 DB 291 SQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGVKORPGHLEWIGDIYPGGGYT 350
 QY 62 YNEKFGKATVTADTSSRTAYVQVRLTSSEDSAVYFCARSAS-----WYF--DVWGARTT 114
 DB 351 YNGKFGKATVTADTSSRTAYVQVRLTSSEDSAVYFCARSATTVGRTYVYAMDYWGQGT 410
 QY 115 VTSSAKTTPKLGDIETQSPKFMSTSGDRVNVYTKASQNV-----GTNVAWFOQKP 170
 DB 411 VTSSAKTTPKLGDIETQSPKFMSTSGDRVNVYTKASQNV-----GTNVAWFOQKP 470
 QY 171 SPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHTYPLTFGGT 230
 DB 471 PPKLLIYDASNLVSGIPRFGSGSGGTDFTLTISNVQSEDIAEYFCQYHTYPLTFGGT 530
 QY 231 KLEIKRADAAGSEQKLISEDLNSHHHHH 262
 DB 531 KLEIKRADAAGSEQKLISEDLNSHHHHH 562
 RESULT 5

QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSESAVYFCARSAS-----WYF--DVWGART 113
 DB 81 NYNGKFGKATLTADSSSTAYVQVRSLSLTSSESAVYFCARETTTTCGRYYVANDYWGQT 140
 QY 114 TTVSSAKTTPKLGDDIELTQSPKFMSTSVGDRVNVYTKASQNVGNVAVFQKPGOSPK 173
 DB 141 SVTVSSAKTTPKLGDDIVLTQSPAINASAPGKVTWTCSSSSV-SYMNWYQKSGTSPK 199
 QY 174 VLYSASRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFTGGTKLE 233
 DB 200 RWIYDTSKLAGVPAHFRGSGGTSYSLTISGMEADAATYCCQWSSNPTFTGGTKLE 259
 QY 234 IKRADAAGSEQKLISEEDLNHHHHH 262
 DB 260 INRADTAPTGEQKLISEEDLNHHHHH 288

RESULT 7

AAW82317
 ID AAW82317 standard; protein; 288 AA.

XX AC AAW82317;

XX DT 26-FEB-1999 (first entry)

XX DE Mouse bispecific antibody variant OKT3/anti-CD19 protein.

XX KW OKT3; monoclonal antibody; Mab; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19;
 KW anti-CD3.

XX OS Mus sp.

XX OS Synthetic.

XX PN DE19721700-Cl.

XX PD 19-NOV-1998.

XX PF 23-MAY-1997; 97DE-01021700.

XX PR 23-MAY-1997; 97DE-01021700.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Kipriyanov S, Little M, Moldenhauer G;

XX DR WPI; 1998-596150/51.
 DR N-PSDB; AAV73337.

XX PT Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced
 PT by another polar amino acid, useful for controlling transplant rejection,
 PT and in tumour diagnostics and therapy.

XX PS Disclosure; Fig 3; 8pp; German.

XX CC This sequence represents a protein which has anti-CD19 activity and is
 CC encoded by a monoclonal antibody (Mab) diabody derived from OKT3 with a
 CC point-mutation where Cys at position H100A is replaced with another polar
 CC amino acid, in this example Ser. The diabody encodes two OKT3 proteins,
 CC one which has anti-CD19 activity and one with anti-CD3 activity. The Mab
 CC is used in lowering or eliminating the transplant rejection in an organ
 CC recipient and for diagnostic methods for tumours and tumour therapy

XX SQ Sequence 288 AA;

Query Match 67.1%; Score 936; DB 2; Length 288;

Best Local Similarity 69.0%; Pred. No. 1e-60;

Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;

QY 1 MAQVLOQSGAELVPGTGVKISCKASGYTFTNYLWGVKORPGHLEWIGDIYVGGYT 60

DB 21 MAQVLOQSGAELVPGTGVKISCKASGYTFTNYLWGVKORPGHLEWIGDIYVGGYT 80

QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSESAVYFCAR--SASWYFDVWGARTTTVS 118
 DB 81 NYNGKFGKATLTADSSSTAYVQVRSLSLTSSESAVYFCARYDDHYSLDYWGQGTTLTVS 140
 QY 119 SAKTTPKLGDDIELTQSPKFMSTSVGDRVNVYTKASQNV-----GTNVAVFQKPGOSPKV 174
 DB 141 SAKTTPKLGDDILLTQTTPASLAVSLGORATISCKASQSDVDYDGDSYLNWYQQIPGQPKL 200
 QY 175 LIYSASRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFTGGTKLEI 234
 DB 201 LIYDASNLYSGVPPRFGSGGTDFTLTINHPVEKVDAAVTHCQOSTEDPWTFTGGTKLEI 260
 QY 235 KRADAAAAGSEQKLISEEDLNHHHHH 262
 DB 261 KRADAAAAGSEQKLISEEDLNHHHHH 288

RESULT 8

AAW82316

ID AAW82316 standard; protein; 288 AA.

XX AC AAW82316;

XX DT 26-FEB-1999 (first entry)

XX DE Mouse OKT3 variant antibody protein.

XX KW OKT3; monoclonal antibody; Mab; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy.

XX OS Mus sp.

XX OS Synthetic.

XX PN DE19721700-Cl.

XX PD 19-NOV-1998.

XX PF 23-MAY-1997; 97DE-01021700.

XX PR 23-MAY-1997; 97DE-01021700.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Kipriyanov S, Little M, Moldenhauer G;

XX DR WPI; 1998-596150/51.
 DR N-PSDB; AAV73335.

XX PT Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced
 PT by another polar amino acid, useful for controlling transplant rejection,
 PT and in tumour diagnostics and therapy.

XX PS Claim 3; Fig 2; 8pp; German.

XX CC This sequence represents a monoclonal antibody (Mab) derived from OKT3
 CC with a point-mutation where Cys at position H100A is replaced with
 CC another polar amino acid, in this example Ser. The Mab is used in
 CC lowering or eliminating the transplant rejection in an organ recipient,
 CC and for diagnostic methods for tumours and tumour therapy

XX SQ Sequence 288 AA;

Query Match 67.1%; Score 936; DB 2; Length 288;

Best Local Similarity 69.0%; Pred. No. 1e-60;

Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;

QY 1 MAQVLOQSGAELVPGTGVKISCKASGYTFTNYLWGVKORPGHLEWIGDIYVGGYT 60

DB 21 MAQVLOQSGAELVPGTGVKISCKASGYTFTNYLWGVKORPGHLEWIGDIYVGGYT 80

QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSESAVYFCAR--SASWYFDVWGARTTTVS 118
 DB 21 MAQVLOQSGAELVPGTGVKISCKASGYTFTNYLWGVKORPGHLEWIGDIYVGGYT 80

QY 115 VTSSAKTPKLGDIETQSPKFMSTSGDRVNVVTKASQNVGTVNVAFFQKPGQSPKV 174
 DB 408 VTSSAKTPKLGDIETQSPKFMSTSGDRVNVVTKASQNVGTVNVAFFQKPGQSPKV 466
 QY 175 LIYSASYRSGVDPDRFTGSGGDFTLTISNVQSEDLAEYFCQOYHTYPLTFCGGTKLEI 234
 DB 467 WIYDTSKLAGSVFAHFRGSGGTSYSLTISGMEADAATYTCQWGSNPFRTGSGTKLEI 526
 QY 235 KRADAAAGSEQKLISEEDLNHHHHH 262
 DB 527 NRADTAPTQSEQKLISEEDLNHHHHH 554

RESULT 11

ID ADR28054

AD 28054 standard; protein; 269 AA.

XX AC

ADR28054;

XX DT

07-OCT-2004 (first entry)

XX DE

NPB polypeptide scFv1, seq id 1.

XX KW

Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;

XX KM

single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX OS

Mus sp.

XX XX

Synthetic.

XX PH

Key Location/Qualifiers

XX FT

Region

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CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.
 XX
 SQ Sequence 269 AA;

Query Match 65.9%; Score 919.5; DB 8; Length 269;

Best Local Similarity 73.6%; Pred. No. 1.5e-59;

Matches 184; Conservative 17; Mismatches 36; Indels 13; Gaps 3;

QY 3 QVQLQSGAEIYRPGTSVKISKASGYTFTNYLWGVKORPGHLEWIGDIYPGGVTNY 62

DB 1 EVQLQSGPELVKPGALVKISKASGYTFTSDINWVKORPGGLEWIGIYFDGSKTKY 60

QY 63 NEKFKGKATVTADTSSRTAYVVRSLTSDSAVYFCARSASWYFDVWGARTTIVTSSAKT 122

DB 61 NEKFKGKATLTVDKSSITVYMLSLTSENSAVYFCARGK-YFDYWGQGTTLTIVTSGGG 119

QY 123 TPKLGG-----DIELTQSPKFMSTSGDRVNVVTKASQNVGTVNVAFFQKPGQSPKV 174

DB 120 GSGGGSGGGGSGALDIVMTQSPKFMSTSGDRVSVTKASQNVATNVAWYQKPGQSPKP 179

QY 175 LIYSASYRSGVDPDRFTGSGGDFTLTISNVQSEDLAEYFCQOYHTYPLTFCGGTKLEI 234

DB 180 LTYSASFSSGVPDRFTGSGGDFTLTISNVQSEDLAEYFCQOYHTYPLTFCGGTKLEI 239

QY 235 KRADAAAGS 244

DB 240 K-----AAAGA 245

AD 28054 standard; protein; 283 AA.

XX ADF85426;

XX AC

XX DT

26-FEB-2004 (first entry)

XX DE

V122scFv clone.

XX KW

Fv library.

XX OS

Unidentified.

XX PN

JP2003334075-A.

XX PD

25-NOV-2003.

XX PF

21-MAY-2002; 2002JP-00145858.

XX PR

21-MAY-2002; 2002JP-00145858.

XX XX

(NISR) JAPAN TOBACCO INC.

XX WPI

2004-027982/03.

XX N-PSDB

ADP85425.

XX FT

Mutated Fv library useful for screening mutated Fv for preparation of

XX FT

mutated antibody for diagnostic purposes, having mutations at specific

XX FT

amino acid positions of complementarity determining regions of antibody.

XX PS

Disclosure; SEQ ID NO 2; 17pp; Japanese.

XX CC

The present invention relates to mutated Fv library having mutations

XX CC

designed such that the amino acid at position k (k is integer 24le;k4le;

XX CC

20) is introduced at amino acid position m (m is integer 24le;m4le;(n-1))

XX CC

chosen from a region consisting of n residues (n is integer 34le;n

XX CC

contained in complementarity determining regions (CDR) or other closer

XX CC

regions of an antibody, and forms limited Fv repertory of (n C m &times

XX CC

;km. The invention can be used for efficiently acquiring mutated

XX CC

antibody. The present sequence represents V122scFv clone.

XX CC

QY 115 VTSSAKTPKLGDIETQSPKFMSTSGDRVNVVTKASQNVGTVNVAFFQKPGQSPKV 174

DB 408 VTSSAKTPKLGDIETQSPKFMSTSGDRVNVVTKASQNVGTVNVAFFQKPGQSPKV 466

QY 175 LIYSASYRSGVDPDRFTGSGGDFTLTISNVQSEDLAEYFCQOYHTYPLTFCGGTKLEI 234

DB 467 WIYDTSKLAGSVFAHFRGSGGTSYSLTISGMEADAATYTCQWGSNPFRTGSGTKLEI 526

QY 235 KRADAAAGSEQKLISEEDLNHHHHH 262

DB 527 NRADTAPTQSEQKLISEEDLNHHHHH 554

AD 28054 standard; protein; 269 AA.

XX AC

ADR28054;

XX DT

07-OCT-2004 (first entry)

XX DE

NPB polypeptide scFv1, seq id 1.

XX KW

Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;

XX KM

single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX OS

Mus sp.

XX XX

Synthetic.

XX PH

Key Location/Qualifiers

XX FT

Region

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XX SQ Sequence 283 AA;
Query Match 65.8%; Score 917.5; DB 8; Length 283;
Best Local Similarity 69.4%; Pred. No. 2.2e-59;
Matches 186; Conservative 21; Mismatches 50; Indels 11; Gaps 3;
QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGMVKQRPCHGLEWIGDIYPCGGYT 60
DB 21 MAQVQLQSGPELVKPGASVMSCKASGYTFSTYMHVWKQKPGQGLEWIGYVNPYNDGI 80
QY 61 NYNEKFKGKATVTADTSSTAYVQVRSLSSEDSAVYFCARSASWYFDVMGARTTIVTSSA 120
DB 81 NYNEKFKGKATLTSKSSATAYMELSLTSDSASVYICARKG---LDYWGQGTITVSSG 137
QY 121 KTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGNVAVFQKPGQSPKV 174
DB 138 GGSAGGGGGGGGSDIELTQSPKFMSTSVGDRVSVTCASQFVGTVMVYQKPGQSPKA 197
QY 175 LIYSASYRYSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQOYHTYPLTGGGTKLEI 234
DB 198 LIYSASTRTGVPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYSSPYTFGSGTKLEI 257
QY 235 KRADAAAAGSEQKLISEEDLNSHHHH 262
DB 258 KRAAGAPVPYDPPL--EPRAHHHHH 283

RESULT 13
ADR70320
ID ADR70320 standard; protein; 267 AA.
XX AC ADR70320;
XX DT 18-NOV-2004 (first entry)
XX DE Poliovirus receptor (PVR)-specific scFv2 protein.
XX KW poliovirus receptor; PVR; CD155; cluster of differentiation 155;
KW receptor mediated adhesion modulation;
KW cell trafficking behaviour modulation;
KW cell invasion behaviour modulation; proliferative disorder; cancer;
KW metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;
KW scFv2.
XX OS Unidentified.
XX PN WO2004074324-A2.
XX PD 02-SEP-2004.
XX PF 19-FEB-2004; 2004WO-EP001637.
XX PR 24-FEB-2003; 2003US-0450064P.
XX PR 28-MAY-2003; 2003EP-00012314.
XX PA (XERI-) XERION PHARM AG.
XX PA (TUFT) UNIV TUFTS.
XX PI Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Jay DG;
PI Eustace BK, Sloan KE;
XX DR WPI; 2004-652917/63.
XX DR N-PSDB; ADR70322.
XX PT New molecules that modulate poliovirus receptor (PVR) mediated adhesion,
PT trafficking and/or invasion behavior of a cell expressing CD155 or PVR,
PT useful for preventing or treating proliferative disorders, such as
PT cancer.
XX PS Claim 7; SEQ ID NO 4; 87pp; English.
XX PT The invention comprises molecules that specifically bind to at least one

CC intra- or extracellular domain of the poliovirus receptor (PVR) - also
CC known as CD155 (cluster of differentiation 155). The molecules of the
CC invention have the ability to modulate receptor mediated adhesion,
CC trafficking and/or invasion behaviour of a cell expressing PVR. The
CC molecules of the invention are useful for the prevention and/or treatment
CC of proliferative disorders, cancer or metastasis. The molecules of the
CC invention are also useful for identifying agents that can modulate PVR-
CC mediated adhesion or invasion potential of cells. The present amino acid
CC sequence represents a PVR-specific scFv protein of the invention.
XX SQ Sequence 267 AA;
Query Match 65.3%; Score 911.5; DB 8; Length 267;
Best Local Similarity 72.8%; Pred. No. 5.8e-59;
Matches 182; Conservative 19; Mismatches 32; Indels 17; Gaps 4;
QY 5 QLQSGAEIVRPGTSVKISKASGYTFNTYWLGMVKQRPCHGLEWIGDIYPCGGYTNNE 64
DB 1 QLQSGPELVKPGASVKISCKTSGYTFETMHWKQSHGKSLWIGGHPNNGDTSYNG 60
QY 65 KFKGKATVTADTSSTAYVQVRSLSSEDSAVYFCARSASWY--FDVMGARTTIVTSSAKT 122
DB 61 RFKKGATLTVDKSSSTAYMELSLTSEDSAVYICAR---WTGDFDYWGQGTITLTVSTGGG 117
QY 123 TPKLGG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGNVAVFQKPGQSPKV 174
DB 118 GSGGGGGGGGSGALDIVMTQSPKFMSTSVGDRVSVTCASQNVGNVAVIQQKPGQSPKA 177
QY 175 LIYSASYRYSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQOYHTYPLTGGGTKLEI 234
DB 178 LIYSASYRYSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYNSYPTTFGGGTKLEI 237
QY 235 KRADAAAAGS 244
DB 238 K----AAAGA 243

RESULT 14
ADP84954
ID ADP84954 standard; protein; 267 AA.
XX AC ADP84954;
XX DT 09-SEP-2004 (first entry)
XX DE Single chain Fv fragment SEQ ID NO 96.
XX KW antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
XX OS Unidentified.
XX PN WO2004050707-A2.
XX PD 17-JUN-2004.
XX PF 01-DEC-2003; 2003WO-DE003994.
XX PR 29-NOV-2002; 2002DE-01056900.
XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
XX PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
PI Christensen PA;
XX DR WPI; 2004-461095/43.
XX PT New recognition molecules, e.g. antibodies (and nucleic acids) that bind
PT specifically to Core-1 antigens, useful for diagnosis, treatment and

prevention of tumors and metastases.
 Claim 26; SEQ ID NO 96; 136pp; German.
 This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IGM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.

Sequence 267 AA;
 Query Match 65.2%; Score 909.5; DB 8; Length 267;
 Best Local Similarity 66.5%; Pred. No. 8.1e-59;
 Matches 179; Conservative 29; Mismatches 40; Indels 21; Gaps 4;

QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNYYLWGKQRPFGHLEWIGDIYPGGYTNY 62
 DB 1 QVQLKESGAELVRPGTSVKISCKASGYTFNYYLWGKQRPFGHLEWIGDIYPGGYTNY 60

QY 63 NEKFKGATVTADTSSTAYVQVRLTSEDSAVYFCARSWSYFDV-----WGARTTV 115
 DB 61 NEKFKGATLTADTSSTAYVQVRLTSEDSAVYFCAR-----YYDAAGPGFAYWGQGTTV 115

QY 116 TVSSAKTTPKLGDIETQSPKFMSTSGVDRVNTYKASQNV-----GTNVANFQOKPGQ 170
 DB 116 TVSSASGSGSSADIQTPTPLSLPVSGLDQASISCRSSQSIHNSNGNTYLEWYLPKPGQ 175

QY 171 SPKVLIIYSASRYSGVDPDRFTGSGSGDTFTLTISNVOSEDIAEYFCQYHYPTLFTGGGT 230
 DB 176 SPKLLIIYKSNRFGVDPDRFGSGSGDTFTLKI SRVEADLGVIYFCQGHVPTFGGT 235

QY 231 KLEIKRADA-----AAAGSEQKLISEEDLN 255
 DB 236 KLEIKRAAAHHHHHGAEGKLISEEDLN 264

RESULT 15
 ADP84957
 ID ADP84957 standard; protein; 264 AA.
 XX ADP84957;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Single chain Fv fragment SEQ ID NO 99.
 XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
 KW

KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
 KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
 KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
 KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
 KW metastasis.
 XX Unidentified.
 OS
 XX WO2004050707-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX 01-DEC-2003; 2003WO-DE003994.
 XX
 PF 29-NOV-2002; 2002DE-01056900.
 XX
 PR (NEMO-) NEMOD BIOTHEAPEUTICS GMBH & CO KG.
 PA
 XX Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
 PI Christensen PA;
 XX
 XX WPI; 2004-461095/43.
 DR
 XX New recognition molecules, e.g. antibodies (and nucleic acids) that bind
 PT specifically to Core-1 antigens, useful for diagnosis, treatment and
 PT prevention of tumors and metastases.
 PT
 XX Claim 26; SEQ ID NO 99; 136pp; German.
 PS
 XX This invention describes novel recognition molecules, especially
 CC antibodies that bind specifically to the Core-1 antigen. The recognition
 CC molecules are used to make constructs containing the framework regions
 CC that separate, include and/or flank the specified sequences, especially
 CC where the framework regions are from the immunoglobulin (Ig) superfamily,
 CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
 CC Most especially the framework regions are from antibodies, particularly
 CC the variable heavy chain (VH) and the variable light chain (VL) of human
 CC and/or murine origin. The constructs may also include a His or myc tag, a
 CC lysine-rich region and/or a multimerisation domain, most particularly it
 CC is a single-chain antibody fragment, multibody, Fab fragment, fusion
 CC protein of an antibody fragment with peptide or protein, and/or an Ig of
 CC types G, M, A, E or D and/or their subclasses. It may be human,
 CC humanised, murine or chimeric, e.g. IGM without the J chain. The
 CC additional sequences/structures in the constructs are Ig domains of
 CC various species, interacting or stabilising domains, signal sequences,
 CC fluorescent dyes, toxins, antibodies with catalytic activity or other
 CC specificities, cytolytic agents, enzymes, immuno-modulators or
 CC effectors, MHC molecules, antigens, chelators for radioactive labels,
 CC liposomes, transmembrane domains, viruses and/or cells, specifically
 CC macrophages. The antibodies, also constructs containing them, nucleic
 CC acid encoding them, and related vectors and host cells, are useful for
 CC prevention (e.g. as vaccine), diagnosis, alleviation, treatment,
 CC monitoring and/or secondary treatment of tumours (specifically of breast,
 CC colon, stomach, pancreas, large/small intestine, ovary, cervix, lung,
 CC prostate, kidney and/or liver) and/or metastases (particularly to liver),
 CC specifically where these are positive for the C1 antigen. The products of
 CC the invention provide simple, reliable and efficient detection of
 CC tumours. They are specific for carcinoma and show almost no binding to
 CC healthy tissue.
 XX
 XX Sequence 264 AA;
 Query Match 64.9%; Score 906; DB 8; Length 264;
 Best Local Similarity 66.5%; Pred. No. 1.5e-56;
 Matches 179; Conservative 30; Mismatches 36; Indels 24; Gaps 5;

QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNYYLWGKQRPFGHLEWIGDIYPGGYTNY 62
 DB 1 QVQLKESGAELVRPGTSVKISCKASGYTFNYYLWGKQRPFGHLEWIGDIYPGGYTNY 60

QY 63 NEKFKGATVTADTSSTAYVQVRLTSEDSAVYFCARSWSYFDV-----WGARTTV 115
 DB 61 NEKFKGATLTADTSSTAYVQVRLTSEDSAVYFCAR-----YYDAAGPGFAYWGQGTTV 115

```
Qy 116 TVSSAKTPEKLGDIETQSPKFMSTSVGDRVNVITYKASQNV-----GTNVAVFQOKPCQ 170
Db 116 TVSSASS--SADIQNTQPLSLPVSIGDQASISCRSSQSIHSHNGNTYLEWYLOKPCQ 172
Qy 171 SPKVLIIYSARYSGVPDRFTGSGGCTDFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGT 230
Db 173 SPKLLIYKVSNRFSGVDPDRFSGSGGCTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGCT 232
Qy 231 KLEIKRADA-----AAGSEQKLISEEDLN 255
Db 233 KLEIKRAAAHHHHHHHGAEQKLISEEDLN 261
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Search completed: February 9, 2006, 03:27:46
Job time : 275.825 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:28:13 ; Search time 25.4654 Seconds
(without alignments)
989.922 Million cell updates/sec

Title: US-10-049-404-2
Perfect score: 1395
Sequence: 1 MAQVQLQSGAEIVRPGETSV.....GSEQKLISEDLNHHHHH 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	50.8	268	A56446	Ig heavy chain V r
2	664.5	47.6	249	S41374	single chain Fv an
3	583.5	41.8	233	JCS322	p53 specific singl
4	570.5	37.3	141	A39276	Ig heavy chain pre
5	516	37.0	121	GWMS11	Ig heavy chain V r
6	501	35.9	115	A56700	Ig heavy chain (an
7	497	35.6	246	S38950	Ig gamma chain - m
8	496	35.6	446	S40295	Ig gamma-2a chain
9	489	35.1	128	A47159	Ig lambda chain V
10	486	34.8	119	PL0089	Ig heavy chain V r
11	486	34.8	136	PL0208	Ig heavy chain pre
12	484	34.7	123	S30560	Ig heavy chain V r
13	482	34.6	119	PL0086	Ig heavy chain V r
14	480	34.4	107	B28195	Ig kappa chain V r
15	478	34.3	108	PL0204	anti-DNA autoantib
16	476	34.1	119	PL0085	Ig heavy chain V r
17	475	34.1	140	PH1482	Ig heavy chain V r
18	472	33.8	117	S42466	Ig kappa chain V r
19	471.5	33.8	116	S53751	antibody Fab Jel 1
20	468.5	33.6	214	PC4202	monoclonal antibod
21	468	33.5	118	S38565	Ig heavy chain V r
22	468	33.5	119	C30562	Ig heavy chain V r
23	467.5	33.5	108	B44371	Ig kappa chain V r
24	467	33.5	138	E32513	Ig heavy chain pre
25	466	33.4	140	T01407	Ig heavy chain (my
26	466	33.4	119	B30562	Ig heavy chain V r
27	464.5	33.3	469	S27483	Ig gamma-2a chain
28	464	33.3	117	MMMS4E	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446

R;Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <FAN>

A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 50.8%; Score 708; DB 2; Length 268;

Best Local Similarity 54.3%; Pred. No. 2e-44;

Matches 146; Conservative 41; Mismatches 64; Indels 18; Gaps 5;

QY	1	MAQVQLQSGAEIVRPGETSVKISKASGYTFTNYLGMVKQRPQGHGLEWIGDIYVGGGYT	60
DB	1	MAQVQLQSGAEIVKPGASVKLSCTTSSTGFKNTYMHVWVKQRPQGLEWIGRIAPANGIT	60
QY	61	NYNEKFKGKATVTADTSSRTAYVQVRSITSEDAVYFCARSASWYF----	DVWGARTVT 116
DB	61	KYDPKFGKATIAADTSSNTAYLQLSLTSEDTAVYVC--ASYLTRYENYWGQGT	117
QY	117	VSS-----AKTTPKLGSDIELTQSPKFMSTSGDRVNVYKASONVGTNVAVFQKPGQ	170
DB	118	VSSGGSGSGGSGGGSDIELTQSPAIMASLGEKVTMCRASSSNVF-IYWTQQKSDA	176
QY	171	SPKVIYASRYSGVDPDRFTGSGSGTDTLTITSNVQSEDLAEYFCQYHTYPTLFGG	230
DB	177	SPKLWYTTSHLPGPVAPFSGSGSGNSYSLTISMEGEDAATYTCQFTSSPTFGSGT	236
QY	231	KLEIKRADA-----AAGSEQKLISEEDLN	255
DB	237	KLEIKRSAHHHHHGAEEQKLISEEDLN	265

RESULT 2

S41374

single chain Fv antibody - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C;Accession: S41374

R;Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A;Description: Construction and functional characterization of a single chain Fv antib

A;Reference number: S41374

A;Accession: A28195
A:Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:G197039; PIDN:AAA38891.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 496; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.8e-29;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 129 DIELTQSPKFMSTVSGDRVNVTKASQNGVTNVANFOQKPGQSPKVIYASRYSGVDP 188
DB 1 DILMTQSPKFMSTVSGDRVSVTKASQNGVGNVAMHQKPGQSPKALIYSASRYSGVDP 60

QY 189 RFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPLTFGGGTKLEIK 235
DB 61 RFTGSGSGTDFLTITINVSQSEDLAEYFCQOYNSYPTTFGGGTKLEIK 107

RESULT 10
A47159
Ig lambda chain V region (CEA-specific maId T84.66) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A47159
R;Gaidd, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A;Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A;Reference number: A47159; MUID:93300804; PMID:7686150
A;Accession: A47159
A;Status: preliminary
A:Molecule type: DNA; protein
A;Residues: 1-128 <GAI>
A;Cross-references: UNIPARC:UPI00001767A5
A;Experimental source: hybridoma 6G6.C4
A;Note: sequence extracted from NCBI backbone (NCBI:134419, NCBI:134420)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 489; DB 2; Length 128;
Best Local Similarity 86.2%; Pred. No. 7.1e-29;
Matches 94; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 128 GDIELTQSPKFMSTVSGDRVNVTKASQNGVTNVANFOQKPGQSPKVIYASRYSGVP 187
DB 20 GDIVLIQSQKFMSTVSGDRVSVTKASQNGVGNVAMVYQKPGQSPKALIYSASRYSGVP 79

QY 188 DFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPLTFGGGTKLEIKR 236
DB 80 DFTGSGSGTDFLTITISNVQSEDLAEYFCQYDNPWTTFGGGTKLEIKR 128

RESULT 11
PL0089
Ig heavy chain V region (12S18-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
C;Accession: PL0089
R;Week, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0089
A:Molecule type: mRNA
A;Residues: 1-119 <MEE>
A;Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:G51591; PIDN:CAA414
A;Note: the sequence shown here is from the VH region of an antidiotypic monoclonal ant
A;Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical to
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 486; DB 2; Length 119;
Best Local Similarity 73.9%; Pred. No. 1.1e-28;
Matches 88; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 3 QVLOQSGAELVRPGTSVKISCKASGYTFTNYWLVGWVKQRPCHGLEWIGDIYPGGGYTN 62
DB 1 QVLOQEPGAELVVKPGASVKMSCKASGYTFTNYWLVGWVKQRPCHGLEWIGDIYPGGGYTN 60

QY 63 NEKFKGKATVTADTSRTAYVQVRLTSDTSVAVFCARSA--SWYFDVMGARTTIVTVSS 119
DB 61 NEKFKSKATLTVDTSSTAYMQISLTSDTSVAVFCARNEGAVAFDVGXGTTVAXSS 119

RESULT 12
PL0208
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C;Accession: PL0208
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacti
A;Reference number: PL0207; MUID:90309764; PMID:1973259
A;Accession: PL0208
A:Molecule type: mRNA
A;Residues: 1-136 <SOU>
A;Cross-references: UNIPARC:UPI0000176C6F
A;Experimental source: hybridoma cell E225
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;118-121/Region: D region
F;122-136/Region: JH region

Query Match 34.8%; Score 486; DB 2; Length 136;
Best Local Similarity 74.6%; Pred. No. 1.3e-28;
Matches 88; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 2 AVOVLQSGAELVRPGTSVKISCKASGYTFTNYWLVGWVKQRPCHGLEWIGDIYPGGGYTN 61
DB 19 SOVLQQPGSELVRPGASVKLSCKASGYTFTNYWLVGWVKQRPCHGLEWIGDIYPGGGYTN 78

QY 62 YNEKFKGKATVTADTSRTAYVQVRLTSDTSVAVFCARSAWYFDVMGARTTIVTVSS 119
DB 79 YDEKFKSKATLTVDTSSTAYMQISLTSDTSVAVFCARGLAFYFDHWGQTTLTVSS 136

RESULT 13
B30560
Ig heavy chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: B30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: B30560
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-123 <MAT>
A;Cross-references: UNIPARC:UPI0000114E20; GB:M24269; NID:G195619; PIDN:AAA38373.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 484; DB 2; Length 123;

Best Local Similarity 77.2%; Pred. No. 1.6e-28;
Matches 95; Conservative 7; Mismatches 15; Indels 6; Gaps 1;
QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNYYLWGVPKPGHLEWIGDIYPGGGYTNV 62
DB 1 QVQLQSGAELVRPGTSVKISCKASGYTFNYYLWGVPKPGHLEWIGDIYPGGGYTNV 60
QY 63 NEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVYFCARSAS-----WYFDVWGARTT 116
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSSPYDYGWYFDVWGARTT 120
QY 117 VSS 119
DB 121 VSS 123

RESULT 14
PL0086
Ig heavy chain V region (E4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0086
R;Week, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0086
A;Molecule type: mRNA
A;Residues: 1-119 <MEE>
A;Cross-references: UNIPARC:UPI0000115F1P; GB:X58595; GB:Y00794; NID:951561; PIDN:CAA414
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal ant
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.6%; Score 482; DB 2; Length 119;
Best Local Similarity 75.6%; Pred. No. 2.1e-28;
Matches 90; Conservative 8; Mismatches 19; Indels 2; Gaps 1;
QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNYYLWGVPKPGHLEWIGDIYPGGGYTNV 62
DB 1 QVQLQSGAELVRPGTSVKISCKASGYTFNYYLWGVPKPGHLEWIGDIYPGGGYTNV 60
QY 63 NEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVYFCAR--SASWYFDVWGARTT 119
DB 61 TORFKAKATLTADKSSSTAYMQLSSLTSDSAVYFCARDDGWSWYFDVWGARTT 119

RESULT 15
B28195
Ig kappa chain V region (anti-haloperidol antibody B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C;Accession: B28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: B28195
A;Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D6A; EMBL:M19767; NID:9197041; PIDN:AAA38892.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 34.4%; Score 480; DB 2; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.6e-28;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 129 DILMTQSKFMSTSVGDRVSVTKASQNVGNVVAHQKPGQSPKALIYSASYRSGVPD 188

DB 1 DILMTQSKFMSTSVGDRVSVTKASQNVGNVVAHQKPGQSPKALIYSASYRSGVPD 60
QY 189 RFTGSGSGTDFTLTITISNVQSEDLAEYFCQQYHTYPLTFGGGTXLEIK 235
DB 61 RFTGSGSGTDFTLTITINVSQEDXAEYFCQQYNSYPYKFGGTXLEIK 107
Search completed: February 9, 2006, 03:34:18
Job time : 26.4654 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 9, 2006, 03:18:36 ; Search time 161.118 Seconds
(without alignments)
1147.288 Million cell updates/sec
Title: US-10-049-404-2
Perfect score: 1395
Sequence: 1 MAQVQLQSGAEIVRPQTSV.....GSRQKLISEDLNHHHHH 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	783.5	56.2	243	2	Q7QM2_MOUSE
2	725.5	52.0	255	2	Q6KB05_MOUSE
3	724	51.9	244	2	Q65ZC8_HUMAN
4	708	50.8	487	2	Q65ZL2_MOUSE
5	669	48.0	240	2	Q65ZC9_HUMAN
6	630	45.2	241	2	Q921A6_MOUSE
7	584.5	41.9	248	2	Q65ZQ7_MOUSE
8	527	37.8	168	2	Q8VDC9_MOUSE
9	520	37.3	468	2	Q569W9_MOUSE
10	516	37.0	121	1	HV01_MOUSE
11	515.5	37.0	218	2	Q925S1_MOUSE
12	514.5	36.9	613	2	Q8VCX7_MOUSE
13	494	35.4	108	2	Q8VIJ0_MOUSE
14	491.5	35.2	143	2	Q91V67_MOUSE
15	483	34.6	238	2	Q58E04_MOUSE
16	479	34.3	473	2	Q8D8L4_MOUSE
17	472	33.8	120	1	HV03_MOUSE
18	470.5	33.7	143	2	Q924Q0_MOUSE
19	467.5	33.5	145	2	Q924R3_MOUSE
20	464.5	33.3	463	2	Q99LC4_MOUSE
21	464	33.3	117	1	HV12_MOUSE
22	464	33.3	144	2	Q924P5_MOUSE
23	464	33.3	458	2	Q5BJ22_RAT
24	463	33.2	117	1	HV13_MOUSE
25	462	33.1	149	1	KV5A_MOUSE
26	462	33.1	486	2	Q5HYZ6_MOUSE
27	460.5	33.0	481	2	Q91WT1_MOUSE
28	459.5	32.9	483	2	Q52L51_MOUSE
29	459	32.9	140	1	HV02_MOUSE
30	457	32.8	470	2	Q7TMK1_MOUSE
31	454.5	32.6	143	2	Q924P9_MOUSE

32	454.5	32.6	143	2	Q924Q5_MOUSE
33	454	32.5	616	2	Q504M7_MOUSE
34	453.5	32.5	590	2	Q4V9V8_MOUSE
35	451	32.3	146	2	Q924R8_MOUSE
36	450	32.3	134	2	Q65ZR6_MOUSE
37	450	32.3	140	2	Q924P8_MOUSE
38	448	32.1	614	2	Q7TWT6_MOUSE
39	447.5	32.1	143	2	Q924R7_MOUSE
40	446.5	32.0	139	1	HV07_MOUSE
41	446	32.0	142	2	Q924Q1_MOUSE
42	445.5	31.9	145	2	Q924Q7_MOUSE
43	445	31.9	464	2	Q6PF95_MOUSE
44	445	31.9	474	2	Q8R3H6_MOUSE
45	443.5	31.8	118	2	Q921C4_MOUSE

ALIGNMENTS

RESULT 1
ID Q7QM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC Q7QM2; 2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ScFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."
RL J. Biol. Chem. 278:36740-36747(2003).
EMBL: AJ574851; CAB00495.1; -; Genomic_DNA.
HSSP; P01751; 1A6W.
DR SMR; Q7QM2; 1-236.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;

Query Match	56.2%;	Score	783.5;	DB 2;	Length	243;			
Best Local Similarity	57.5%;	Pred. No.	5.4e-56;						
Matches	153;	Conservative	34;	Mismatches	50;	Indels	29;	Gaps	4;
Qy	3	QVQLQSGAEIVRPQTSVKISKASGYTFYTWLGNWYKQRFPGHGLEWIGDIYPGGGYTNY	62						
Db	1	QVQLQSGSELVRPGASVKLSCASGYFTFYWVHWYKQKHGQGLEWIGNIYPGSGITNY	60						
Qy	63	NEKFKGATVTADTSSRTAYVQVRSLSLTSDESAVYFCARSAWYFDVWGARTTIVTSSAKT	122						
Db	61	DEKFNKGILTVDTSSSTAYMHLSSLASEDSAVVYCARGGRG-LDVWGAGITLTIVSSGGG	119						
Qy	123	TPKLGG-----DIELTQSPKFMSTSVCDRVNVIKASQNVGTNVAWFOQKPGQSPKVL	176						
Db	120	GSGGGGGGGGSDIQMTQSSSFSVSLGRVTITCKASEDINRLAWYQKPGNAPRL	179						
Qy	177	YSASRYSGVDRFTGSGSGDFTLTISNVQSEDLAIFYCOQHYTYPLTFGGGKLEIKR	236						
Db	180	SGATSLGTGVSRFSGSGSKDYLTLSITSLQTEDVATYCCQYWS-TRTFGGGKLEIK-	237						
Qy	237	ADAAAAGSEQKLISEEDLNLSHHHHH	262						

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Db 238 -----HHHHH 243

RESULT 2
Q6KB05_MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; A4746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; IKCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 52.0%; Score 725.5; DB 2; Length 255;
Best Local Similarity 52.2%; Pred. No. 3.2e-51;
Matches 144; Conservative 37; Mismatches 58; Indels 37; Gaps 4;

QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPGLHLEWIGDIYPGGGYTNV 62
Db 1 QVQLQSGGDLVPGGSLVKSCASGFTFSSYGMKSWRQTPDKRLHVAITISGGSYTY 60

QY 63 NEKFKGKATVADTSSRTAYVQVRSITSDSAVYFCAASW----YFDVWGARTTIVTS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYCARHINRYDCAFYWGQGTTLTVS 120

QY 119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYKASQ-----NVGTNVAWFOQ 166
Db 121 SGGGSGGGGGGGSDIVMAQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQ 180

QY 167 KPQSPKVLIVYASVRYSGVDPDFTGSGGTDFLTISNVQSEDLAEYFCQYHYTPTLF 226
Db 181 KPQSPKLLIYGASTRESGVDPDFTGSGGTDFLTISNVQSEDLAEYFCQYHYTPTLF 240

QY 227 GGGTKLEIKRAAAAAAGSEQKLISEEDLNSHHHHH 262
Db 241 GAGTKLEIK-----HHHHH 255

RESULT 3
Q65ZC8_HUMAN
ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

Db 238 -----HHHHH 243

Query Match 51.9%; Score 724; DB 2; Length 244;
Best Local Similarity 57.4%; Pred. No. 4e-51;
Matches 140; Conservative 39; Mismatches 55; Indels 10; Gaps 2;

QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPGLHLEWIGDIYPGGGYTNV 62
Db 1 QVQLVQSGAEVKKPGQSVVKVCKASGYTFSDHYMHVVRQAPGGLEWGWIDPNNGDTRF 60

QY 63 NEKFKGKATVADTSSRTAYVQVRSITSDSAVYFCAR----SASWYFDVWGARTTIVTS 118
Db 61 AQRFGQGVMTTRDTSISAAVMEVSRLSDDTAVYVCAREGTGSAIYGMVDVWGQGTTLTVS 120

QY 119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYKASQNVGTNVAWFOQKPGQSP 172
Db 121 SGGGSGGGGGGGSDIQMTQSPSTLSASIGDVRVITCRASEGIYHVAWYQQKPKGAP 180

QY 173 KVLIVYASVRYSGVDPDFTGSGGTDFLTISNVQSEDLAEYFCQYHYTPTLF 232
Db 181 KFLIVYASSLASGAPSRFSGSGGTDFLTISLQPDPTATYCCQYSNYPLTFGGGTGL 240

QY 233 EIKR 236
Db 241 EIKR 244

RESULT 4
Q65ZL2_9MURI
ID Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN-<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
GO; GO:0003823; Fc antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
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DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 50.8%; Score 708; DB 2; Length 487;
Best Local Similarity 56.7%; Pred. No. 1.9e-49;
Matches 139; Conservative 37; Mismatches 49; Indels 20; Gaps 3;

QY 2 AQVQLQSGAELVRPGTSVKISCKASGYTFNTYWLGNVQKRPQGHLEWICDIYPGGGYTN 61
DB 19 SQVQLQSGAELVRPGTSVKISCKASGYTFDTHAIHWAKQPEQGLEWIGYISPGNDDIK 78
QY 62 YNEKFKGKATVTADTSSRTAYVQVRSITSDSAVYFCARSASWYFDVWGARTTIVTSSAK 121
DB 79 YNEKFKGKATLTADKSSSTAYMQLNSITSDSAVYFCARS---YGHWGQGTTLTGSGG- 134
QY 122 TTPKLG-----IELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQ 170
DB 135 -----GGSGGGSGGGSGRIQMTQSPASLSVSGELVITTCRASENIYSLNLAWYQOKQK 189
QY 171 SPKVLVYSARYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIFYCQOYHTYPLTFGGGT 230
DB 190 SPQLVYATNLADGVPSRFSGGSGGTQYSLKINSQSEDVFGSYCQHFVGTFTYFGGT 249
QY 231 KLEIK 235
DB 250 RLEIK 254

RESULT 5
Q65ZC9 HUMAN
ID Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9_2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Names=acFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
ON NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbr0797-629;
RA Kontermann R.E., Ming M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 48.0%; Score 669; DB 2; Length 240;
Best Local Similarity 54.2%; Pred. No. 1.3e-46;
Matches 130; Conservative 37; Mismatches 67; Indels 6; Gaps 1;

QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNTYWLGNVQKRPQGHLEWIGDIYPGGGYTN 62
DB 1 QVQLVQSGGGLVQPGGSLRISCAASGFTFSYGMHWVRQAPGKLEWAVISYDGSNKY 60

QY 63 NEKFKGKATVTADTSSRTAYVQVRSITSDSAVYFCARSASWYFDVWGARTTIVTSSAKT 122
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCARDWGSGLDPWGKGLTIVTSSGGG 120
QY 123 TTPKLG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSPKVL 176
DB 121 GSGGGSGGGSGGSDIQMTQSPSTLSASIGDRVITTCRASGIYRWLAWYQOKPGKAPKLL 180
QY 177 YSASVRYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIFYCQOYHTYPLTFGGGTLEIKR 236
DB 181 YKASSLASRAPRFRSGSGSGTDTLTISLQPDPAFYICQOYSNYPLTFGGGTLEIKR 240

RESULT 6
Q921A6 MOUSE
ID Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6_2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DE 01-DEC-2004 (T-EMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWV.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 45.2%; Score 630; DB 2; Length 241;
Best Local Similarity 52.1%; Pred. No. 2e-43;
Matches 126; Conservative 37; Mismatches 71; Indels 8; Gaps 3;

QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNTYWLGNVQKRPQGHLEWIGDIYPGGGYTN 62
DB 1 QVQLQSGGPELKKPGETVKISCKASGYTFDYGMWVQAPGKLGWGWINTTGTPTY 60
QY 63 NEKFKGKATVTADTSSRTAYVQVRSITSDSAVYFCAR-SASWYFDVWGARTTIVTSSAK 121
DB 61 ADFFKGRFAPSLTSTASTAYLQINLNKNEDTAYFCARDLLRYFDYWGQGTITVTVSSGG 120
QY 122 TTPKLG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSPKVL 175
DB 121 GSGGGSGGGSGGSDIELTQSPSSLSASLGKGVITTCASQDINKYIAWYQHKPGKPRSA 180


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RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -; mRNA.
DR HSP; P01665; 1ONZ.
DR Ensembl; ENSMUSG0000058040; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 23013 MW; 52784FA8F7982817 CRC64;

Query Match 37.0%; Score 515.5; DB 2; Length 218;
Best Local Similarity 50.7%; Pred. No. 4.2e-34;
Matches 110; Conservative 33; Mismatches 57; Indels 17; Gaps 5;

QY 1 MAQVQLQDSGAELVRPGTSVKISKASGYTFNYLWLGWVKQRPCHGLEWIGDIYPGGYT 60
Db 1 MAQVQLQDSGAELVRPGTSVKISKASGYTFNYLWLGWVKQRPCHGLEWIGDIYPGGYT 60

QY 61 NYNEKFKGKATVTADTSSTRTAYVQVRSLSLTSSEDSAVYFCARSASWYFD----VWGARTT 116
Db 61 NYNEKFKGKATVTADTSSTRTAYVQVRSLSLTSSEDSAVYFCARSASWYFD----VWGARTT 116

QY 117 VSSAKTTPKLG-----DIETQSPKFMSTSGVDRVNTYKASQ---NVGN-NVAFQ 166
Db 117 VSSAKTTPKLG-----DIETQSPKFMSTSGVDRVNTYKASQ---NVGN-NVAFQ 166

QY 167 KQSQSKVLIVSYASYSGVDPDRFTGSGSGTDFTLI 203
Db 167 KQSQSKVLIVSYASYSGVDPDRFTGSGSGTDFTLI 203

QY 178 KPGQPPKLLIYAASKQSGVPGAGLIASGSGTDFSLNI 214
Db 178 KPGQPPKLLIYAASKQSGVPGAGLIASGSGTDFSLNI 214

RESULT 12
QY 12
ID Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Names=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauniger R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2464031;
RA Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1---6)dextran.";
RL J. Immunol. 142:888-893(1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR FIR; C30562; C30562.
DR HSP; P01751; LA6W.
DR Ensembl; ENSMUSG0000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0003033; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 36.9%; Score 514.5; DB 2; Length 613;
Best Local Similarity 79.8%; Pred. No. 1.8e-33;
Matches 95; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 2 AQVQLQDSGAELVRPGTSVKISKASGYTFNYLWLGWVKQRPCHGLEWIGDIYPGGYT 61
Db 19 SQVQLQDSGAELVKPGASVKISCKATGYTFSSWIEWVKQRPCHGLEWIGDIYPGGSSTN 78

QY 62 YNEKFKGKATVTADTSSTRTAYVQVRSLSLTSSEDSAVYFCARS-ASWYFDVWGARTT 119
Db 79 YNEKFKGKATVTADTSSTRTAYVQVRSLSLTSSEDSAVYFCARRLGRWYFDVWGARTT 137

RESULT 13
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AC Q8VJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Names=Igh-V19-14; Synonyms=Vk19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
FN	[1]
RN	NUCLEOTIDE SEQUENCE.
RP	STRAIN=C57BL/6;
RA	Kozono Y., Kozono H., Azuma T.;
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RR	EMBL; AB069912; BAB63928.1; -; mRNA.
DR	EMBL; AB069914; BAB63930.1; -; mRNA.
DR	PIR; S26744; S26744.
DR	HSP; P01V75; 1A6W.
DR	SMR; Q91V67; 1-129.
DR	Ensembl; ENSMUSG0000021155; Mus musculus.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
FT	NON TER 1
FT	NON TER 143
FT	SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;
QY	Query Match 35.2%; Score 491.5; DB 2; Length 143;
DB	Best Local Similarity 78.0%; Pred.No. 2.3e-32;
DB	Matches 92; Conservative 9; Mismatches 16; Indels 1; Gaps
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Dy	1 QVQLQQSGAEIVRGTSVKISCKASGYTFTSYNMHWVKQRPGGLEWIGVIDPSDSYNY 6
Qy	63 NEKPKGKATVTADTSSRTAVQVRSITSEDSAVVFCARSA-SWYFDVMGARTTTVSS 119
Dy	61 NQPKFGKATVTDTSSSTAYWLSSLTSEDSAVVYCPTDDWFYDWGTGTTTVSS 118
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ID	Q58EU4_MOUSE PRELIMINARY; PRT; 238 AA.
AC	Q58EU4;
DT	10-MAY-2005 (TrEMBLrel. 30, Created)
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE	Igk-C protein.
GN	Name=Igk-C.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridea; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RC	NUCLEOTIDE SEQUENCE.
RP	STRAIN=FVB/N; TISSUE=Colon;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klauster R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Alecuth S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA	Schneer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RC NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091754; AAH91754.1; -; mRNA.
DR SMR; Q58EU4; 25-238.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 238 AA; 26440 MW; AE2B2BA90B9F7D5D CRC64;

Query Match 34.6%; Score 483; DB 2; Length 238;
Best Local Similarity 82.3%; Pred. No. 2.1e-31;
Matches 93; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

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24 GDIVMTQSHKFMSTSGDRVSIICKASQDVTTAVAWYQQKPGQSPKVLIIHWASTRHTGVP 83

Qy 188 DRFTGSGSGTDFLTITISNVQSEDLAEYFCQQVHTYPLTFGGGKLEIKRADAA 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 DRFTGSGSGTDFLTITISNVQSEDLADYFCQQYSSYPLTFGSGTKLEIKRADAA 136

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 Job time : 165.118 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
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(without alignments)
622.979 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867.5	62.2	288	2	US-09-423-439-38
2	862.5	61.8	249	1	US-08-797-689-18
3	862.5	61.8	249	2	US-09-984-186-18
4	858	61.5	240	2	US-10-096-246A-35
5	856	61.4	240	2	US-10-092-246-36
6	856	61.4	240	2	US-10-096-246A-37
7	853	61.1	240	2	US-10-092-246-35
8	848	60.8	240	2	US-10-096-246A-36
9	841	60.3	240	2	US-10-092-246-37
10	819.5	58.7	239	2	US-10-092-246-33
11	819.5	58.7	239	2	US-10-096-246A-33
12	814.5	58.4	257	2	US-10-092-246-2
13	814.5	58.4	257	2	US-10-096-246A-2
14	813	58.3	240	2	US-10-096-246A-34
15	811	58.1	264	2	US-10-114-716A-46
16	808	57.9	240	2	US-10-092-246-34
17	804.5	57.7	239	2	US-10-092-246-32
18	804.5	57.7	239	2	US-10-096-246A-32
19	798.5	57.2	246	1	US-08-469-486-57
20	798.5	57.2	246	1	US-08-469-658-57
21	786.5	56.4	673	2	US-09-423-439-37
22	783.5	56.2	355	2	US-08-875-811-57
23	779	55.8	269	2	US-08-646-265A-109
24	774	55.5	258	2	US-09-526-738A-4
25	766	54.9	273	1	US-08-403-853-18
26	765.5	54.9	250	1	US-08-133-804-2
27	765.5	54.9	250	1	US-08-461-184-8

28	765.5	54.9	250	1	US-08-463-675-8	Sequence 8, Appli
29	765.5	54.9	250	1	US-08-464-589-8	Sequence 8, Appli
30	765.5	54.9	250	1	US-08-461-838-2	Sequence 2, Appli
31	765.5	54.9	250	1	US-08-461-386-2	Sequence 2, Appli
32	765	54.8	256	2	US-09-526-738A-2	Sequence 10, Appl
33	764	54.8	271	1	US-08-894-922A-10	Sequence 10, Appl
34	760.5	54.5	267	2	US-09-419-788-30	Sequence 22, Appl
35	760	54.5	288	2	US-09-818-247-22	Sequence 16, Appl
36	759.5	54.4	553	1	US-08-661-052-16	Sequence 16, Appl
37	759.5	54.4	553	2	US-09-188-082-16	Sequence 16, Appl
38	759.5	54.4	553	2	US-09-364-088-16	Sequence 16, Appl
39	759.5	54.4	553	2	US-09-102-716-16	Sequence 19, Appl
40	758.5	54.4	483	1	US-08-392-338A-19	Sequence 19, Appl
41	758.5	54.4	483	2	US-09-166-750-19	Sequence 19, Appl
42	758.5	54.4	483	2	US-09-166-093-19	Sequence 19, Appl
43	758.5	54.4	483	2	US-09-172-019-19	Sequence 19, Appl
44	758.5	54.4	483	2	US-09-166-094-19	Sequence 19, Appl
45	758.5	54.4	483	2	US-09-443-213-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match	62.2%	Score	867.5	DB 2	Length	288			
Best Local Similarity	62.8%	Pred. No.	5.7e-63						
Matches	174	Conservative	35	Mismatches	43	Indels	25	Gaps	5
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Db	21	MAQVLOQPGAELVKPGASVOLSKASGYTFTGWIHWKORPGGLEWIGVNPSTGRS	80						
Qy	61	NYNEKFKGKATVTADTSRTAYQVRSITSDESAVYFCARSASWYF----	116						


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DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVVFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSNTVMQLSSLTSEDVAVVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDRVNVVTKASQNVGTVNAVFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPNSLSTSGDRIRITCKASQDVDTAVGWYQQRPGQSPKL 178
QY 175 LIYSASYRYSVGPDRFTGSGSGDTFTLTISNQVSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSSTRHTGVDPDRFTGSGSGDTFTLTISNQVSEDLADYFCHQYSSHPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
```

```
RESULT 7
US-10-092-246-35
; Sequence 35, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35
```

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Query Match 61.1%; Score 853; DB 2; Length 240;
Best Local Similarity 68.6%; Pred. No. 6.9e-62;
Matches 166; Conservative 25; Mismatches 43; Indels 8; Gaps 2;
QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYMLGWVKQRPGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVVFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSNTVMQLSSLTSEDVAVVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDRVNVVTKASQNVGTVNAVFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPKFMSTSGDRIRITCKASQDVDTAVGWYQQRPGQSPKL 178
QY 175 LIYSASYRYSVGPDRFTGSGSGDTFTLTISNQVSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSSTRHTGVDPDRFTGSGSGDTFTLTISNQVSEDLADYFCHQYSSHPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
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```
RESULT 8
US-10-096-246A-36
; Sequence 36, Application US/10096246A
; Patent No. 6818748
```

```
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal scFv Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-36
```

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Query Match 60.8%; Score 848; DB 2; Length 240;
Best Local Similarity 68.6%; Pred. No. 1.8e-61;
Matches 166; Conservative 24; Mismatches 44; Indels 8; Gaps 2;
QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYMLGWVKQRPGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVVFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSNTVMQLSSLTSEDVAVVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDRVNVVTKASQNVGTVNAVFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPNSLSTSGDRIRITCKASQDVDTAVGWYQQRPGQSPKL 178
QY 175 LIYSASYRYSVGPDRFTGSGSGDTFTLTISNQVSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSSTRHTGVDPDRFTGSGSGDTFTLTISNQVSEDLADYFCHQYSSHPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
```

```
RESULT 9
US-10-092-246-37
; Sequence 37, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37
```

```
Query Match 60.3%; Score 841; DB 2; Length 240;
Best Local Similarity 68.2%; Pred. No. 6.6e-61;
Matches 165; Conservative 24; Mismatches 45; Indels 8; Gaps 2;
QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYMLGWVKQRPGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
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[illegible]

RESULT 10
 US-10-092-246-33
 ; Sequence 33, Application US/10092246
 ; Patent No. 6501314
 ; GENERAL INFORMATION:
 ; APPLICANT: The Minister of National Defence, Government of Canada
 ; APPLICANT: Fulton, R E
 ; APPLICANT: Alvi, Azhar E
 ; APPLICANT: Nagata, Leslie
 ; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
 ; TITLE OF INVENTION: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
 ; FILE REFERENCE: NEL-0007
 ; CURRENT APPLICATION NUMBER: US/10/092,246
 ; CURRENT FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Mouse hybridoma cell line 1A4A1
 ; US-10-092-246-33

	Query Match	58.7%;	Score 819.5;	DB 2;	Length 239;
	Best Local Similarity	67.4%;	Pred. No. 3.7e-59;		
	Matches 163;	Conservative	24;	Mismatches 46;	Indels 9; Gaps 3;
Qy	1	MAQVQLQSGAGLELVRPGTSVKISKCKASGYTFDTHVHWKVPKQGLEWIGDIYPGGGYT	60		
Db	1	MAQVQLQSGGPELVKPGASVKISKCKASGYTFDTHVHWKVPKQGLEWIGMTYPGPDPT	60		
Qy	61	NYNEKPKGKATVTADTTSRTAYVQVRSLTSDSAVYFCARSASWYFDVWGARTTIVTVSSA	120		
Db	61	NYSETFGKATLTVDTSNTVYMQLLSLLTSDTAVYFCARGVG--LDYWGQGGTIVTVSSG	118		
Qy	121	KTTPLKG-----DIELTQSPKWSISVGRVNVYTKASNVGNTVAWFOQKQSPKV	174		
Db	119	GGSGGGGGGGGGSDSSSLVS--KPVTSISGRIRITCKASQDVADVAVGVIQQRPGQSPKL	177		
Qy	175	LIYASVRYSGVPRDFRTGSGSGDTFTLTISNVQSEDLAIEYFCQGYHTYPLTFGGGTKLEI	234		
Db	178	LIYGSSTWYAVRPFRTGSGSGDTFTLTISNVQSEDIADYFCHOYSSYPFTFGSGTKLEI	237		

RESULT 11
US-10-096-246A-33
; Sequence 33, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of

```

; TITLE OF INVENTION: Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 239
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-33

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Query Match	58.7%;	Score	819.5;	DB 2;	Length	239;			
Best Local Similarity	67.4%;	Pred. No.	3.7e-59;						
Matches	163;	Conservative	24;	Mismatches	46;	Indels	9;	Gaps	3
Qy	1	MAQVQLQDGGAEIVRPGTSVKISKASGYFTFTNYLWLGKVRKORPGHGLEWIGDIYPGGCGYT	60						
Db	1	MAQVQLQDSGPELVKPGASVKISKASGYFTTDTHVHWVKGKPGQGLEWIGMTYFGPPDT	60						
Qy	61	NYNEKFGKATVTADTSSRTAYVQVRSLTSDSAVYFCARSASWYFDVMGARTTTVTVSSA	120						
Db	61	NYSETFGKATLTVDTSNTVYMQLSLTSDTADVYFCARGVG--LDYMGQGTIVTVSSG	118						
Qy	121	KTTPKLGQ-----DIETLQSPKFMSTSGDVRNVNVTYKASQNVGNTNVAMFOOKPQGS	174						
Db	119	GGSGGGGGGGGSDSSSLVS-KFVSTSIGDRIRITCKASQDVTAVGWYQORPQSPKL	177						
Qy	175	LIYSASRYRSGVDPDRFTFGSGSGDTFTLTISNVQSEDLAEYFCQQYHTVPLTFGGGKTLEI	234						
Db	178	LI FWSSTRHTGVDPDRFTFGSGSGDTFTLTISNVQSEDLADEYCHQVSSYPFTFGSGKTLEI	237						
Qy	235	KR	236						
Db	238	KR	239						

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RESULT 12
US-10-092-246-2
; Sequence 2, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Negata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Function
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encep
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
; US-10-092-246-2

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	Query Match	58.4%;	Score 814.5;	DB 2;	Length 257;
	Best Local Similarity	66.0%;	Pred. No. 1e-58;		
	Matches 163;	Conservative 25;	Mismatches 50;	Indels 9;	Gaps 3;
Qy	1	MAQVQLQSGAEIIVRGTSVKIKSCASGYFTFTNYLWGVKQRPQGHLEWIGDIYPGGGYT	60		
Db	1	MAQVQLQSGPELVKPGASVKISCKASGYFTDTHHWKVKPKQGLEWIGMTYPPGPDNT	60		
Qy	61	NYNEKFKGKATVTADTSSRTAYVQVRLSTSDSAVYFCARSAWYFDVWGARTTTVTSSA	120		
Db	61	NYSETFKGKATLVDTFTSTVYMQLSLTSIEDTVVYFCARGVG--LDYWGQGTITVTSSG	118		
Qy	121	KTTPKLG-----DIELTQSPKFMSTSGVDRVNVITYKASQNVGTINVAWFQOKPQSPKV	174		

Qy

63

NEKPKGKATVTADTSSTAYVQVRSLTSEDSAVYFCARSASWYFDVWGARTTIVTS SAKT

122

Db

61

NQKFKSKATLTVDKSSSTAYMELHSLTSEDSAVYFCARFSS--FDYWGQGTIVTVSSG--

116

Qy

123

TPKLGG-----DIELTQSPKFMSTSVGDRVNVITYKASONVGTNVAVFQOKPGQ

170

Db

117

---GGGGGGVGGGGGSDIQMTQSPSSLASLGDTTITICHASONINWLSWYQOKPGN

172

Qy

171

SPKVLIIYSASYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOQVHTYPLTFGGGT

230

Db

173

IPKLLIYRASNLHTGVPSRFGSGSGTGFTLTISLQPEDIAITYCQOQGSYPLTFGTGT

232

Qy

231

KLEIKRADA---AAAGSEQKLISEEDLN

255

Db

233

KLEIKRAAAHHHHHHHGAEQKLISEEDLN

261

Search completed: February 9, 2006, 03:35:34

Job time : 35.7701 secs

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; Publication No. US20050118569A1
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie P.
; APPLICANT: Alvi, Azhar Z.
; APPLICANT: Hu, Wei-Gang
; TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged
; TITLE OF INVENTION: Single-Chain Variable Fragment Antibody to Venezuelan Equine
; FILE REFERENCE: NEL-0018
; CURRENT APPLICATION NUMBER: US/10/784,305
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: 60/448,902
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: scfv: 1-269;
; OTHER INFORMATION: SBP,6His and spacers: 270-296
; US-10-784-305-2

Query Match 63.9%; Score 891.5; DB 5; Length 296;
Best Local Similarity 64.8%; Pred. No. 8.7e-60;
Matches 177; Conservative 26; Mismatches 57; Indels 13; Gaps 3;

QY 1 MAQVQLQDSGAEIVRGTSTVKISKASGYFTFTNYLWLVKQKPGHLEWIGDIYPGGVT 60
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 26 MAQVQLQDSGPELVKPGASVKISKASGYFTFDYHVHVKPGQGLEWIGMTPGFDNT 85
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 NYNEKFKGKATVTDTSRTAYVQVRSLSVTSASVYFCARSASWYFDVAGRTVTVSSA 120
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 86 NYSETFGKATLVDTSSNTVYVQVRSLSVTSASVYFCARGVG--LDYWGQGTITVTVSSG 143
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 KTTPTKLG-----DIELTQSPKFMSTSVGDRVNVVTKASQNVGTINVAWFQKPGQSPKV 174
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 144 GGGSGGGGGGGSDIELTQSPNSLSTSGDRIRITCKASQDVDTAVGWYQKPGQSPKL 203
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 175 LIYSASYRYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFTGGGKLEI 234
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 204 LIPWSSTRHTGVDPDRFTGSGSGDTFTLTISNVQSEDLADYFCHQYSGSPFTFTGSGTKLEI 263
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 235 KRADAAGS-----EQKLISEEDLNSHHHHH 262
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 264 KRAAHSGGGGCPCHPQPPRCYAGGGGSHHHHH 296
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 3
US-10-984-186-18
; Sequence 18, Application US/09984186
; Patent No. US2002015101A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
; US-09-984-186-18

Query Match 61.8%; Score 862.5; DB 3; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQDSGAEIVRGTSTVKISKASGYFTFTNYLWLVKQKPGHLEWIGDIYPGGVTNY 62
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 4 QVQLQDSGPELVKPGASVKISKASGYAFSRSMWVVKQKPGGLEWIGRIYFGDGTKY 63
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 NEKEFKGKATVTDTSRTAYVQVRSLSVTSASVYFCARSAS-----WYEDVWGARTTV 115
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 64 NKFGKATLVTDTSRTAYVQVRSLSVTSASVYFCAKENRFDERGYAMDIWGGTIV 123
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVVTKASQNVGTINVAWFQKPG 169
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 124 TVSSGGGGGGGGGGGSGGSGNIQLTQSPNSMSTSVGDRVSIITCKASQDVDTSVAVYQKPG 183
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 170 QSPKVLIIYSARYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFTGGG 229
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 184 QSPKLLIYWASTRTHTGVDPDRFTGSGSGDTFTLTISNVQSEDSADYFCQYSSYPWTFGGG 243
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 230 TKLEIK 235
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 244 TKLEIK 249
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 4
US-10-237-667-18
; Sequence 18, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
```

```

;
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
;
; US-10-237-667-18
;
; Query Match 61.8%; Score 862.5; DB 4; Length 249;
; Best Local Similarity 69.5%; Pred. No. 1.2e-57;
; Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;
;
; Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNYWLGWVKQRPCHGLEWIGDIYPCGGYTN 62
; Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLEWIGRIYPGDGTKY 63
;
; Qy 63 NEKPKGATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 115
; Db 64 NGKPKGATLTADRSSSTAYWQLSSLTSVGSAYVFCAKENRPFDERGYANDYWGQGTIV 123
;
; Qy 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVITYKASQNVGTNVAVFQKPG 169
; Db 170 QSPKVLIVSAYRYSGVPDRFTGSGGTDFTLTISNQVSEDLAYFCQOYHYTPLTFGGG 229
;
; Qy 184 QSPKLLIYWASTRTGTVPDRFTGSGGTDFTLTISNQVSEDSADYFCQOYSSYPWTFGGG 243
;
; Qy 230 TKLEIK 235
; Db 244 TKLEIK 249
;
; RESULT 5
; US-10-237-708-18
; Sequence 18, Application US/10237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
;
;
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,708
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
;
; US-10-237-708-18
;
; Query Match 61.8%; Score 862.5; DB 4; Length 249;
; Best Local Similarity 69.5%; Pred. No. 1.2e-57;
; Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;
;
; Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNYWLGWVKQRPCHGLEWIGDIYPCGGYTN 62
; Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLEWIGRIYPGDGTKY 63
;
; Qy 63 NEKPKGATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 115
; Db 64 NGKPKGATLTADRSSSTAYWQLSSLTSVGSAYVFCAKENRPFDERGYANDYWGQGTIV 123
;
; Qy 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVITYKASQNVGTNVAVFQKPG 169
; Db 170 QSPKVLIVSAYRYSGVPDRFTGSGGTDFTLTISNQVSEDLAYFCQOYHYTPLTFGGG 229
;
; Qy 184 QSPKLLIYWASTRTGTVPDRFTGSGGTDFTLTISNQVSEDSADYFCQOYSSYPWTFGGG 243
;
; Qy 230 TKLEIK 235
; Db 244 TKLEIK 249
;
; RESULT 6
; US-10-237-708-18
; Sequence 18, Application US/10237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
;
;

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US-10-237-866-18
; Sequence 18, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA: US/10/237,866
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 249 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-866-18
Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAELVPGTSTKISKASGYFTFTNWLGVKQRPQGHLEWIGDIYPGGGYTNV 62
DB 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLEWIGRIYPGDGTKY 63
QY 63 NEKFKGKATVADTSRTAYQVRSITSDSAVYFCARSAS-----WYFDVWGARTTV 115
DB 64 NGKFKGKATLTADRSSSTAYMQLSSITSVGSAVYFCAKENNRFDERYGYAMDYWGQGTTV 123
QY 116 TVSSAKTPKLG-----DIETQSPKEMSTSVGDRVNVYKASQNVGTNVAWFOQKPG 169
DB 124 TVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 183
QY 170 QSPKVLIIYASRYSGVPRFTGSGSGTDTFTLTISNVQSEDLAEYFCQQYHTYPLTFGGG 229
DB 184 QSPKLLIYNASTRTGVPDRFTGSGSGTDTFTLTISNVQSEDSADYFCQQYSSYPWTFGGG 243

US-10-237-871-18
; Sequence 18, Application US/10237871
; Publication No. US20030036172A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA: US/10/237,871
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 249 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-871-18
Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAELVPGTSTKISKASGYFTFTNWLGVKQRPQGHLEWIGDIYPGGGYTNV 62
DB 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLEWIGRIYPGDGTKY 63
QY 63 NEKFKGKATVADTSRTAYQVRSITSDSAVYFCARSAS-----WYFDVWGARTTV 115
DB 64 NGKFKGKATLTADRSSSTAYMQLSSITSVGSAVYFCAKENNRFDERYGYAMDYWGQGTTV 123
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US-10-702-536-18

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Query Match      61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVPSTSVKISKASGYTFTNVLGWVKORPGHLEWIGDIYVGGYTNV 62
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKORPGGLEWIGRIYVPGDGTKY 63

QY 63 NEKFKGKATVADTSRTAYVQVRSITSDSAVYFCARSAS-----WVFDVWGARTTV 115
Db 64 NGKFKGKATLTADRSSTAYMQLSLTSVGSAYVFCAKENRDEYGYAMDYWGQTTV 123

QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTNVAWFQKPG 169
Db 124 TVSSGGGGSGGGGGGSGNSIQLTQSPNSMSTSVGDRVSIITCKASQDVTSTVAWYQKPG 183

QY 170 QSPKVLISASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAIEYFCQYHTYPLTFGGG 229
Db 184 QSPKLLIYWASTRHTGVDPDRFTGSGSGTDFTLTISNVQSEDSADYFCQYSSYPWTFGGG 243

QY 230 TKLEIK 235
Db 244 TKLEIK 249
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RESULT 10

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US-10-702-636-18
; Sequence 18, Application US/10702636
; Publication No. US20040086977A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Jean-Dominique
; Guitton, Alain
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
```

```
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10702,636
FILING DATE: 06-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
```

```
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-702-636-18
```

```
Query Match      61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVPSTSVKISKASGYTFTNVLGWVKORPGHLEWIGDIYVGGYTNV 62
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKORPGGLEWIGRIYVPGDGTKY 63

QY 63 NEKFKGKATVADTSRTAYVQVRSITSDSAVYFCARSAS-----WVFDVWGARTTV 115
Db 64 NGKFKGKATLTADRSSTAYMQLSLTSVGSAYVFCAKENRDEYGYAMDYWGQTTV 123

QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTNVAWFQKPG 169
Db 124 TVSSGGGGSGGGGGGSGNSIQLTQSPNSMSTSVGDRVSIITCKASQDVTSTVAWYQKPG 183

QY 170 QSPKVLISASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAIEYFCQYHTYPLTFGGG 229
Db 184 QSPKLLIYWASTRHTGVDPDRFTGSGSGTDFTLTISNVQSEDSADYFCQYSSYPWTFGGG 243

QY 230 TKLEIK 235
Db 244 TKLEIK 249
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RESULT 11

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US-11-146-077-18
; Sequence 18, Application US/11146077
; Publication No. US20050239167A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/146,077
; FILING DATE: 07-JUN-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
```

FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-11-146-077-18

Query Match 61.8%; Score 862.5; DB 6; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;
QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPQGHLEWIGDIYPGGGYTN 62
Db 4 QVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPQGHLEWIGDIYPGGGYTN 63
QY 63 NEKPKGKATVTADTSSRTAYVQVRSLSSEDSAVYFCARSAS-----WYFVVGARTTV 115
Db 64 NGPKGKATVTADTSSRTAYVQVRSLSSEDSAVYFCARSAS-----WYFVVGARTTV 123
QY 116 TVSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNTYKASQNVGTNVAVFQKPG 169
Db 124 TVSSGGGGGGGGGGGSGNSQLTQSPNSMSTSVGDRVNTYKASQNVGTNVAVFQKPG 183
QY 170 QSPKVLISYRSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYHTYPLTFGGG 229
Db 184 QSPKLLIYASTRTGVPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYHTYPLTFGGG 243
QY 230 TKLEIK 235
Db 244 TKLEIK 249

RESULT 12
US-10-378-832A-2
Sequence 2, Application US/10378832A
Publication No. US20040005333A1
GENERAL INFORMATION:
APPLICANT: Her Majesty the Queen in right of Canada, as represented by the Minister
of National Defence
APPLICANT: Negata, Leslie P
APPLICANT: Fulton, R. Elaine
APPLICANT: Hu, Weigang
APPLICANT: Alvi, Azhar Z
TITLE OF INVENTION: No. US20040005333A1el Fusion Protein of Human IgG1 Heavy Chain Co
FILE REFERENCE: NEL-0013
CURRENT APPLICATION NUMBER: US/10/378,832A
CURRENT FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 622
TYPE: PRT
ORGANISM: mouse hybridoma cells and human lymphocytes
US-10-378-832A-2

Query Match 61.8%; Score 862.5; DB 4; Length 622;
Best Local Similarity 68.7%; Pred. No. 3.1e-57;
Matches 171; Conservative 24; Mismatches 43; Indels 11; Gaps 3;
QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPQGHLEWIGDIYPGGGYTN 60
Db 60 MAQVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPQGHLEWIGDIYPGGGYTN 119

QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTVTVSSA 120
Db 120 NYSETEKFGKATVTADTSSRTAYVQVRSLSSEDSAVYFCARGVG--LDYWGQGTITVTVSSG 177
QY 121 KTPPKLGG-----DIETQSPKFMSTSVGDRVNTYKASQNVGTNVAVFQKPGQSPKV 174
Db 178 GGGSGGG 237
QY 175 LIYSASRYSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYHTYPLTFGGGTKLEI 234
Db 238 LIYWSSTRTGVPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYHTYPLTFGGGTKLEI 297
QY 235 KRADAAAAG 243
Db 298 KR--AAAG 303

RESULT 13
US-10-511-794-21
Sequence 21, Application US/10511794
Publication No. US20050158322A1
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
FILE REFERENCE: 976-20 PCT/US
CURRENT APPLICATION NUMBER: US/10/511,794
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/CU2003/000005
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: CU2002/0086
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 21
LENGTH: 255
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: diabody MS
US-10-511-794-21

Query Match 61.4%; Score 856.5; DB 5; Length 255;
Best Local Similarity 65.2%; Pred. No. 3.4e-57;
Matches 172; Conservative 27; Mismatches 52; Indels 13; Gaps 5;
QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFNTYWLGVKQRPQGHLEWIGDIYPGGGYTN 62
Db 1 EVKLIVSGGDLVKPGGSLKFSKASGPPFNRYAMSWYRQTPKGLWVAFI--SSDGIAYY 59
QY 63 NEKPKGKATVTADTSSRTAYVQVRSLSSEDSAVYFCAR---SASWYFDVWGARTTVTVSS 119
Db 60 ADSVKGRFTISRDNRNAILYQLMSLSKSEDTAMTCARVYYSYSGYFDYWGQGTITVTVSS 119
QY 120 AKTTPKLGDIETQSPKFMSTSVGDRVNTYKASQNVGTNVAVFQKPGQSPKVLIIYSA 179
Db 120 GGG---GSDILMTQSPKFMSTSVGDRVNTYKASQNVGTNVAVFQKPGQSPKVLIIYSA 175
QY 180 SYRSGVDPDRFTGSGSGTDFLTISNVQSEDLAEYFCQYHTYPL--TFGGGTKLEIKRAD 238
Db 176 SSRNSGVDPDRITGSGSGTDFLTISNVQSEDLAEYFCQYHTYPLTFGGGTKLEIK--- 232
QY 239 AAAAGSEQLISEEDLNHHHHH 262
Db 233 -AAAGSEQLISEEDLNHHHHH 255

RESULT 14
US-10-096-246-36
Sequence 36, Application US/10096246
Publication No. US2003010060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada

```
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mouse
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-36
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Query Match 61.4%; Score 856; DB 4; Length 240;
Best Local Similarity 69.0%; Pred. No. 3.5e-57;
Matches 167; Conservative 24; Mismatches 43; Indels 8; Gaps 2;
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QY 1 MAQVQLQSGAEIVRFGTSVKISKASGYFTFTNYLWGVKORPGHGLEWIGDIYPCGGYT 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MAQVQLQESGPELVKPGASVKISKASGYFTTDYHVHWKPGQGLEWIGMTYPCGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVOVRSLSLTSSEDSAVYFCARSASWYFDVWGARTTIVTSSA 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NYSETFKGKATLTVDTSSTNTVMQLSSLTSEDYAVYFCARGVG--LDYWGQGGTTVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQOKPGQSPKV 174
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GGGSGGGGGGGSDIELTQSPNLSLTSIGDRIRITCKASQDVDTAVGVYQORPGQSPKL 178
QY 175 LIYSASYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOYHYTPLTFGGGTKLEI 234
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
179 LIFWSTRHTGVDPDRFTGSGGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLEI 238
QY 235 KR 236
Db ||
239 KR 240
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RESULT 15
US-10-096-246-35
; Sequence 35, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mouse
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-35
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Query Match 61.1%; Score 853; DB 4; Length 240;
Best Local Similarity 68.6%; Pred. No. 5.9e-57;
Matches 166; Conservative 25; Mismatches 43; Indels 8; Gaps 2;
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QY 1 MAQVQLQSGAEIVRFGTSVKISKASGYFTFTNYLWGVKORPGHGLEWIGDIYPCGGYT 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MAQVQLQESGPELVKPGASVKISKASGYFTTDYHVHWKPGQGLEWIGMTYPCGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVOVRSLSLTSSEDSAVYFCARSASWYFDVWGARTTIVTSSA 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 61 NYSETFKGKATLTVDTSSTNTVMQLSSLTSEDYAVYFCARGVG--LDYWGQGGTTVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQOKPGQSPKV 174
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GGGSGGGGGGGSDIELTQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQOKPGQSPKL 178
QY 175 LIYSASYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOYHYTPLTFGGGTKLEI 234
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
179 LIFWSTRHTGVDPDRFTGSGGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLEI 238
QY 235 KR 236
Db ||
239 KR 240
```

```
Search completed: February 9, 2006, 03:59:47
Job time : 123.43 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:55:47 ; Search time 19.0991 Seconds
(without alignments)
180.014 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVQLQSGAEIVRPGTSV.....GSEQLISEEDLNHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	805.5	57.7	615	6	US-10-512-184-50
2	800	57.3	290	7	US-11-032-773-957
3	793.5	56.9	543	6	US-10-495-664-3
4	790.5	56.7	319	7	US-11-032-773-955
5	779	55.8	269	6	US-10-839-799-109
6	765.5	54.9	245	7	US-11-054-515-1902
7	763.5	54.7	251	7	US-11-054-515-1921
8	760.5	54.5	592	6	US-10-016-686-4
9	759	54.4	248	7	US-11-054-515-1778
10	757	54.3	248	7	US-11-054-515-1008
11	755.5	54.2	243	6	US-10-016-686-1
12	755.5	54.2	247	7	US-11-054-515-3242
13	751.5	53.9	488	6	US-10-016-686-3
14	748	53.6	242	7	US-11-054-515-1915
15	747	53.5	244	7	US-11-054-515-1881
16	745	53.4	248	7	US-11-054-515-1446
17	741.5	53.2	249	7	US-11-054-515-926
18	738	52.9	250	7	US-11-054-515-932
19	737.5	52.9	249	7	US-11-054-515-918
20	736	52.8	248	7	US-11-054-515-1104
21	734	52.6	246	7	US-11-054-515-1920
22	731.5	52.4	241	7	US-11-054-515-1577
23	731.5	52.4	249	7	US-11-054-515-1635
24	728.5	52.2	249	7	US-11-054-515-919
25	728	52.2	248	7	US-11-054-515-1717

26 727.5 52.2 243 7 US-11-054-515-2063 Sequence 2063, Ap
27 727 52.1 242 7 US-11-054-515-1580 Sequence 1580, Ap
28 727 52.1 246 7 US-11-054-515-2062 Sequence 2062, Ap
29 726 52.0 248 7 US-11-054-515-1700 Sequence 1700, Ap
30 726 52.0 248 7 US-11-054-515-1719 Sequence 1719, Ap
31 726 52.0 248 7 US-11-054-515-1733 Sequence 1733, Ap
32 726 52.0 248 7 US-11-054-515-1737 Sequence 1737, Ap
33 726 52.0 248 7 US-11-054-515-1879 Sequence 1879, Ap
34 725.5 52.0 241 7 US-11-054-515-1948 Sequence 1948, Ap
35 724.5 51.9 245 7 US-11-054-515-1900 Sequence 1900, Ap
36 724.5 51.9 248 6 US-10-512-184-36 Sequence 36, Appl
37 724 51.9 248 7 US-11-054-515-1771 Sequence 1771, Ap
38 721.5 51.7 241 6 US-10-902-546-6 Sequence 6, Appl
39 721.5 51.7 245 7 US-11-054-515-1972 Sequence 1972, Ap
40 718 51.5 245 6 US-10-512-184-48 Sequence 48, Appl
41 715.5 51.3 247 7 US-11-054-515-969 Sequence 969, Appl
42 714.5 51.2 257 7 US-11-056-825-10 Sequence 10, Appl
43 712 51.0 626 6 US-10-512-184-49 Sequence 49, Appl
44 711.5 51.0 241 6 US-10-902-546-5 Sequence 5, Appl
45 711.5 51.0 243 7 US-11-054-515-1943 Sequence 1943, Ap

ALIGNMENTS

RESULT 1

US-10-512-184-50

; Sequence 50, Application US/10512184

; Publication No. US2005024901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

; TITLE OF INVENTION: resistance against fungi

; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 50

; LENGTH: 615

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: fusion protein

; OTHER INFORMATION: comprising the leader peptide - chitinase - linker

; OTHER INFORMATION: - scfV S22 - cmc/His6.

US-10-512-184-50

Query Match 57.7%; Score 805.5; DB 6; Length 615;
Best Local Similarity 59.6%; Pred. No. 2.1e-48;
Matches 165; Conservative 35; Mismatches 58; Indels 19; Gaps 6;

Qy 1 MAQVQLQSGAEIVRPGTSVKISCKASGYTFTNNVLGVKVRQPHGLEWIGDIYVGGYIT 60
Db 342 MAQVQLQSGTGLARPCASVKMSCKASGYTFTSYMMHWKVRQPGGLEWIGAIYFGSNDT 401

Qy 61 NYNEKPKGKATVADTSSRTAYQVRSITQSDSAVYFCARSASWYF--DVWGARTTVTS 118
Db 402 SYNQKPKGKAKLTAVTSTSTAYMELSLTNEDSAVYICRT-DWDYAMDYWGQGTSTVTS 460

Qy 119 SAKT-----TPKLGDIILTQSPKFMSTSVGDRVNVITYKASQNVGTNVAWFOOK 167
Db 461 SGSTSGSGKPGPGEGSTGKGPADIVLFQSPVIMASPGKVTMTCSASSV-NIYIYQWK 519

Qy 168 PGQSPKVLIIYSASRYSGVPRFTGSGSGDTFTLTISNVOSEDLAEPCCQHYVPLTFG 227
Db 520 SGTSFKRWIYDTSKLAGSGVPVRFSGSGSTFSLTISSEAEADITATYCCQWSSPPLTFG 579

Qy 228 GGTKLEIKRADAAGSEOKLISEEDLNS--HHHHH 262

Db 580 AGTKLEIKRAVDAAA--EQKLISEEDLGALDHHHHH 614

```
RESULT 2
US-11-032-773-957
; Sequence 957, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD SIC5 V5 His protein sequence
US-11-032-773-957

Query Match      57.3%; Score 800; DB 7; Length 290;
Best Local Similarity 58.4%; Pred. No. 2.5e-48;
Matches 170; Conservative 31; Mismatches 60; Indels 30; Gaps 7;

QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYLWLVGWKQRPCHGLEWIGDIYPCGGYT 60
D* 1 MAEVQLQSGAEIVKPGASVKISKASGYTFTDHIHVVYKQRPQGLEWIGFISPGNGDI 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRLTSEDSSAVYFCARSASW-----YFDVWGARTT 116
L* 61 RYNEKFKDKATLTADKSSSTAYMQVSLTSDSVAVYFCARGNTVVVYTDYWGQGTIT 120
QY 117 VSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYTKASQNV-----GTNVAMFQK 164
Db 121 VSSS-GAPGGGGGGGGGGSDIVLTQSPALMSASLEERVMTCTASSSVSSSYFHWY 179
QY 165 QQKPGSPKVLIIYSARYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOYHTYPL 224
Db 180 QQKPGSPKLIWYTTNLSAGVPAFPFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPLTF 239
QY 225 TFGGGTKLEIKRADA-----AAGS-----EQKLISEEDLNS-----HHHHH 262
Db 240 TFGAGTKLEIKRADAAPTVAASFLGKPIPNPLGLDSTNSAVDHHHHH 290

RESULT 3
US-10-495-664-3
; Sequence 3, Application US/10495664
; Publication No. US20050244416A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, GUNDRAM
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
; FILE REFERENCE: 034258-0801
; CURRENT APPLICATION NUMBER: US/10/495,664
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match      56.9%; Score 793.5; DB 6; Length 543;
Best Local Similarity 59.1%; Pred. No. 1.2e-47;
Matches 162; Conservative 26; Mismatches 55; Indels 31; Gaps 4;

QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFTNYLWLVGWKQRPCHGLEWIGDIYPCGGYTNY 62
Db 287 QVQLQSGPELVKPGASVKISKASGYAFSRSMWVWVQRPQGLEWIGRIYPGDGTNY 346
QY 63 NEKFKGKATVTADTSSRTAYVQVRLTSEDSSAVYFCARS-----ASWYFDVWGARTT 118
Db 347 NGKFKGKATLTADKSSSTAYMQVSLTSDSVAVYFCARGNTVVVYTDYWGQGTIT 406
QY 119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYTKASQNV-----GTNVAMFQK 168
Db 407 SGGGGGGGGGGGGSDIVLTQSPALMSASLEERVMTCTASSSVSSSYFHWY 466
QY 169 QQSPKVLIIYSARYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOYHTYPLTF 228
Db 467 QQPPKLLIYASNLSEGVPAFPFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPLTF 526
QY 229 GTKLEIKRADAAGSEQKLISEEDLNSHHHHH 262
Db 527 GTKLEIKRAA-----HHHHH 543

RESULT 4
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD SIC5 CD20 His Protein Sequence
US-11-032-773-955

Query Match      56.7%; Score 790.5; DB 7; Length 319;
Best Local Similarity 53.4%; Pred. No. 1.2e-47;
Matches 171; Conservative 31; Mismatches 59; Indels 59; Gaps 7;

QY 1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYLWLVGWKQRPCHGLEWIGDIYPCGGYT 60
Db 1 MAEVQLQSGAEIVKPGASVKISKASGYTFTDHIHVVYKQRPQGLEWIGFISPGNGDI 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRLTSEDSSAVYFCARSASW-----YFDVWGARTT 116
Db 61 RYNEKFKDKATLTADKSSSTAYMQVSLTSEDSSAVYFCARGNTVVVYTDYWGQGTIT 120
QY 117 VSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYTKASQNV-----GTNVAMFQK 164
Db 121 VSSS-GAPGGGGGGGGGGSDIVLTQSPALMSASLEERVMTCTASSSVSSSYFHWY 179
QY 165 QQKPGSPKVLIIYSARYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOYHTYPL 224
Db 180 QQKPGSPKLIWYTTNLSAGVPAFPFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPLTF 239
```



```
RESULT 7
US-11-054-515-1921
; Sequence 1921, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1921

Query Match          54.7%; Score 763.5; DB 7; Length 251;
Best Local Similarity 59.4%; Pred. No. 6.9e-46;
Matches 149; Conservative 34; Mismatches 51; Indels 17; Gaps 2;

QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTNY 62
DB 1 QVQLVQSGAEVKPGASVKVCKASGYTFSTYGISWVRQAPGGQGLEWGMGWSAYNGENTY 60
QY 63 NEKPKGKATVTADTSRTAYVQVRSLTSEDSAVYFCARSASY-----FDVWGA 111
DB 61 AQKLRGRVTMTDTSTSTAYMELRSLRSDDTAVYCARVTSLSYSSSSGGYTYGMDVWGR 120
QY 112 RTTIVTSSAKTTPKLAG-----DIETQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQ 165
DB 121 GTTIVTSSGGGGGGGGGGGGSDIQMTQSPSLASVGRVVTTCRASQGINNYLAWYQ 180
QY 166 QKPGQSPKVLIVSASRYSGVDPDRFTGSGSGTDTLTITISNVQSEDLAEYFCQYHTYPLT 225
DB 181 QKPGRAPKLLIYAASSLQGVSPRSFSGSGSGTDTLTITISLQPEDFATYYCYLQDSYPLT 240
QY 226 FGGGTTKLEIKR 236
DB 241 FGGGTTKLEIKR 251

RESULT 8
US-10-016-686-4
; Sequence 4, Application US/10016686
; Publication No. US20060014222A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
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; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carrol, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the Ig-5T4 fusion protein
US-10-016-686-4

Query Match          54.5%; Score 760.5; DB 6; Length 592;
Best Local Similarity 62.0%; Pred. No. 2.4e-45;
Matches 152; Conservative 28; Mismatches 56; Indels 9; Gaps 2;

QY 2 AQVQLQSGAELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 61
DB 19 SEVQLQSGPDLVLPFGASVKISCKASGYSTGYVHWVWKQSHGKSLIEWIGRINPNNGVT 78
QY 62 YNEKPKGKATVTADTSRTAYVQVRSLTSEDSAVYFCARS---ASWYFDVWGARTVTYVS 118
DB 79 YNQKPKDKAILLVDSSTTAYMELRSLTSEDSAVYFCARSTMTITNVMDYNGQVTSVTVS 138
QY 119 S-----AKTTPKLGDIELTQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQKPGQSP 172
DB 139 SGGGGGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDVAVYQKPGQSP 198
QY 173 KVLIVSASRYSGVDPDRFTGSGSGTDTLTITISNVQSEDLAEYFCQYHTYPLTFCGGTKL 232
DB 199 TLLISYTSRYAGVDPDRFTGSGGYGDTFTTISTLQEDLAVYFCQDQVNSPPTFGGGTKL 258

QY 233 EIKRA 237
DB 259 EIKRA 263

RESULT 9
US-11-054-515-1778
; Sequence 1778, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
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QY 234 IKR 236
Db 241 IKR 243

RESULT 12
US-11-054-515-3242
; Sequence 3242, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3242
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3242

Query Match 54.2%; Score 755.5; DB 7; Length 247;
Best Local Similarity 58.7%; Pred. No. 2.4e-45;
Matches 145; Conservative 38; Mismatches 51; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGHWKVRPGHLEWIGDIYPGGYTNY 62
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTILGNYISWVRQAPGGGLEWMGAILPNFTTNY 60

QY 63 NEKFKGKATVTADTSSRTAYQVRSITSEDSAVYFCARSA-----WYFDVWGARTTV 115
Db 61 VQKFGQGVMTTDTSTAYMELRSRSDTAVYCYCARGSSGWYDYIYMDVWGKGTWV 120

QY 116 TVSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVYKASQNVGTNNVAMFOQKPG 169
Db 121 TVSSGGGGGGGGGGGGSDIQMTQSPFSLASIGDRVITTCRASEGIYHWLAWYQKPG 180

QY 170 QSPKVLAYSARYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHYTPTFGGG 229
Db 181 KAPKLLIYKASSLASGAPSRFSGSGGDTFTLTISLQPDDFATYCYQYSNYPFLTGGG 240

QY 230 TKLEIKR 236
Db 241 TKLEIR 247

RESULT 13
US-10-016-686-3
; Sequence 3, Application US/10016686
; Publication No. US20060014222A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingsman, Alan
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion protein
US-10-016-686-3

Query Match 53.9%; Score 751.5; DB 6; Length 488;
Best Local Similarity 61.7%; Pred. No. 8.3e-45;
Matches 150; Conservative 28; Mismatches 56; Indels 9; Gaps 2;

QY 2 AQVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGHWKVRPGHLEWIGDIYPGGYTNY 61
Db 246 SEVQLQSGPDLVKGPGASVKISKASGYSTGYMHWKVKSHGKSLIEWIGRINPNNGVTL 305

QY 62 YNEKFKGKATVTADTSSRTAYQVRSITSEDSAVYFCARS---ASWYFDVWGARTTVTVS 118
Db 306 YNQKPKDKAILTVDKSSTTAYMELRSITSEDSAVYCARSTMITNYMDYWGQVTSVTVS 365

QY 119 S-----AKTTPKLGDIETQSPKFMSTSVGDRVNVYKASQNVGTNNVAMFOQKPGQSP 172
Db 366 SGGGGGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPGQSP 425

QY 173 KVLIIYSARYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHYTPTFGGGTKL 232
Db 426 TLLISYTSRYAGVDPDRFTGSGYGTDTFTTISTLQAEIDLAVYFCQDYNSPPTFGGGTKL 485

QY 233 EIK 235
Db 486 EIK 488

RESULT 14
US-11-054-515-1915
; Sequence 1915, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1915
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1915

Query Match      53.5%  Score 748; DB 7; Length 242;
Best Local Similarity 59.9%; Pred. No. 7.6e-45;
Matches 145; Conservative 3; Mismatches 52; Indels 8; Gaps 2;

QY      3 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 62
Db      1 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 60
QY      63 NEKPKGKATVADTSSRTATVQVRSLSYVFCARSAWYF--DVGARTTIVTSSA 120
Db      61 AQKFGQGRVTITADKSTSTAYMELSLRSDDTAVYICARPSYIYMAVWGQGLTVTVSSG 120
QY      121 KTFPKLGG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFQKPGQSPKV 174
Db      121 GGGSGGGGGGGGSDIQMTQSPSLASVGDRTVITCRASQGINNYLAWYQKPGRAPKL 180
QY      175 LIYSASVRYSGVPRFTGSGSGDTFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGTXLEI 234
Db      181 LIYAASLSQSGVPRFSGSGSDTFTLTISLQPEDFATYYCQDSDYPLTFGGGTXLEI 240
QY      235 KR 236
Db      241 KR 242

RESULT 15
US-11-054-515-1881
; Sequence 1881, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-11-054-515-1881

Query Match      53.5%  Score 747; DB 7; Length 244;
Best Local Similarity 59.4%; Pred. No. 9e-45;
Matches 145; Conservative 42; Mismatches 47; Indels 10; Gaps 3;

QY      3 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 62
Db      1 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 60
QY      63 NEKPKGKATVADTSSRTATVQVRSLSYVFCARSAWYF--DVGARTTIVTSS 118
Db      61 AQKFGQGRVTITADKSTSTAYMELSLRSDDTAVYICARPSYIYMAVWGQGLTVTVSSG 120
QY      119 SAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFQKPGQSP 172
Db      121 SGGSGGGGGGGGSDIVMTQSPSTLSASVGDRTVITCRASQGINNYLAWYQKPGRAPK 180
QY      173 KVLIIYSASVRYSGVPRFTGSGSGDTFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGTXL 232
Db      181 KLIIYAASLSQSGVPRFSGSGSDTFTLTISLQPEDFATYYCQDSDYPLTFGGGTXV 240
QY      233 EIKR 236
Db      241 EIKR 244

Search completed: February 9, 2006, 04:00:31
Job time : 20.0991 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:18:06 ; Search time 281.675 Seconds
(without alignments)
425.847 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQQSGAELRPGASV.....GSEQKLISDELNSHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1470	100.0	273	4 AAB70763	Aab70763 Single ch
2	1231.5	83.8	272	7 ADE22203	Ade22203 Multivale
3	1041.5	70.9	415	2 AAR56484	Aar56484 Scfv PRAS
4	1027.5	69.9	402	2 AAR56485	Aar56485 Scfv PRAS
5	1026.5	69.8	269	2 AAR54756	Aar54756 PRAS111 b
6	1025.5	69.8	269	2 AAR56482	Aar56482 Scfv PRAS
7	1015.5	69.1	256	2 AAR22568	Aar22568 ScfvB18 c
8	1014.5	69.0	256	2 AAR22584	Aar22584 Scfv PRAS
9	1014.5	69.0	435	2 AAR56483	Aar56483 Scfv PRAS
10	1011.5	68.8	256	2 AAR22582	Aar22582 ScfvB18 c
11	1010.5	68.7	428	2 AAR24027	Aar24027 Single ch
12	1010.5	68.7	443	2 AAR24025	Aar24025 Single ch
13	1009.5	68.7	256	2 AAR22587	Aar22587 ScfvB18 c
14	1009.5	68.7	256	2 AAR22585	Aar22585 ScfvB18 c
15	1008.5	68.6	256	2 AAR22586	Aar22586 ScfvB18 c
16	1005.5	68.4	256	2 AAR22583	Aar22583 ScfvB18 c
17	862	58.6	562	6 ABR57059	AbR57059 Plasmid p
18	834.5	56.8	239	8 ADT07625	AdT07625 Polypepti
19	825	56.1	288	2 AAW58826	Aaw58826 Human CD3
20	824.5	56.1	288	2 AAW82317	Aaw82317 Mouse bis
21	824.5	56.1	288	2 AAW82316	Aaw82316 Mouse OKT
22	821.5	55.9	243	8 ADT07627	AdT07627 Polypepti
23	807.5	54.9	288	2 AAW82482	Aaw82482 Mouse bis
24	799.5	54.4	539	3 AAY50823	Aay50823 Fv-antibo

ALIGNMENTS

RESULT 1

AAB70763

ID AAB70763 standard; protein; 273 AA.

XX AAB70763;

DT 18-MAY-2001 (first entry)

DE Single chain Fv antibody construct anti-CD30 VL domain protein.

XX Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
KW tumor cell; natural killer cell activation; Hodgkin's disease;
KW Reed-Sternberg disease.

OS Synthetic.

XX DE199337264-A1.

XX 15-FEB-2001.

XX 06-AUG-1999; 99DE-01037264.

XX 06-AUG-1999; 99DE-01037264.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;

XX WPI; 2001-184000/19.

PT New Fv-antibody construct, useful for treating Hodgkin and Reed-Sternberg
PT diseases, has binding sites for CD16 receptor and CD30 surface protein.

XX Disclosure; Page 11; 18pp; German.

XX This invention describes a novel Fv-antibody construct (1) having binding
XX sites for a CD16 receptor and a CD30 surface protein. The invention also
XX describes (1) expression vector encoding (1); (2) transformants
XX containing the vector of (1); (3) preparation of (1) by culturing cells
XX of (2); and (4) kit comprising (1) and/or the vector of (1), and
XX auxiliaries such as buffers, solvents, carriers, controls and labels, or
XX their replacements. The products of the invention have cytostatic
XX activity. (1) causes lysis of CD30+, specifically tumor, cells. It
XX activates natural killer cells, through the CD16 receptor, and directs
XX them to CD30-expressing cells. (1) are used to treat diseases in which
XX CD30+ cells are implicated, particularly tumors and specifically Hodgkin

Aay50822 Fv-antibo
Adz26387 MOP11 ant
Adr42630 Mouse ant
Adm32742 Amino aci
Aab70762 Single ch
Aap80157 Biosynthe
Aeb29087 Immunokin
Ade29202 Multivale
Abr57058 Plasmid p
Ades2216 E3Bi prot
Ades2217 pGLEN-EH3
Ades2214 pGLEN-EH3
Aaw82743 Fusion pr
Adq91100 Antibody
Adq91082 Antibody
Adq91092 Antibody
Adq91080 Antibody
Adq91090 Antibody
Abb07680 MOGxCD3 f
Ada14263 Human MOG
Adq91106 Antibody

25 799.5 54.4 554 3 AAY50822
26 786.5 53.5 294 9 ADZ26387
27 785.5 53.4 539 8 ADR42630
28 774 52.7 267 8 ADM32742
29 771.5 52.5 262 4 AAB70762
30 759 51.6 240 1 AAP80157
31 754 51.3 594 9 AEB29087
32 753.5 51.1 264 7 ADE29202
33 751 51.1 562 6 ABR57058
34 739 50.3 574 7 ADE2216
35 735 50.0 2606 7 ADE2217
36 735 50.0 2606 7 ADE2214
37 730 49.7 288 2 AAW82743
38 709 48.2 492 8 ADQ91100
39 707 48.1 492 8 ADQ91082
40 707 48.0 492 8 ADQ91092
41 706 48.0 492 8 ADQ91080
42 705 48.0 492 8 ADQ91090
43 704 47.9 409 5 ABB07680
44 704 47.9 409 6 ADA14263
45 704 47.9 492 8 ADQ91106

CC or Reed-Sternberg diseases. (I) have a stronger lytic action than known
 CC bispecific antibodies, can be produced on a large scale with high purity,
 CC and contain no components that can induce unwanted immune responses
 XX
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1470; DB 4; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4.2e-93;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVQLQSGAEELARPGASVKMSCKASGYTFYTIHWVRQRPGLDLEWIGYINPSSGYS 60
 DB 1 MAQVQLQSGAEELARPGASVKMSCKASGYTFYTIHWVRQRPGLDLEWIGYINPSSGYS 60
 QY 61 DYNQNFPGKTTLTADKSSNTAYMQLNSLTSDSAVYVCARRADYGNVYTWFAWQGGTT 120
 DB 61 DYNQNFPGKTTLTADKSSNTAYMQLNSLTSDSAVYVCARRADYGNVYTWFAWQGGTT 120
 QY 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180
 DB 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180
 QY 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHHVFGGTT 240
 DB 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHHVFGGTT 240
 QY 241 KLTVLGQPKSAAGSEQKLISEEDLNSHHHHH 273
 DB 241 KLTVLGQPKSAAGSEQKLISEEDLNSHHHHH 273

RESULT 2
 ADE29203
 ID ADE29203 standard; protein; 272 AA.

XX AC ADE29203;
 XX DT 29-JAN-2004 (first entry)
 XX DE Multivalent multimeric antibody CD19xCD16 related protein 3.
 XX KW multivalent multimeric antibody; bispecific diabody; BsbD;
 KW human B cell marker; CD19; human Fc gamma receptor III; CD16; cytostatic;
 KW immunosuppressive; B-cell malignancy; non-Hodgkin lymphoma;
 KW B-cell mediated autoimmune disease; B-cell depletion; immune response;
 KW human anti-murine antibody response; CD19 x CD16 BsbD; pSKID19x16; mouse;
 KW murine.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= Complementarity_determining_region_H1
 FT Region 50..56
 FT /label= Complementarity_determining_region_H2
 FT Region 99..113
 FT /label= Complementarity_determining_region_H3
 FT Region 124..133
 FT /label= Synthetic_linker
 FT Region 158..171
 FT /label= Complementarity_determining_region_L1
 FT Region 187..196
 FT /label= Complementarity_determining_region_L2
 FT Region 226..234
 FT /label= Complementarity_determining_region_L3
 FT Region 255..264
 FT /label= c-myc epitope
 FT Region 267..272
 FT /label= 6xHis_tag
 XX EP1314741-A1.
 XX PN 28-MAY-2003.

XX 14-NOV-2001; 2001EP-00127061.
 XX 14-NOV-2001; 2001EP-00127061.
 XX (AFFI-) AFFIMED THERAPEUTICS AG.
 XX Le Gall F, Kipriyanov MS, Moldenhauer G, Little M, Cochlovius B,
 PI Schaefer JH;
 XX WPI; 2003-620028/59.
 DR N-PSDB; ADE29201.
 XX Multivalent multimeric antibody for treating B-cell malignancies such as
 PT non-Hodgkin lymphoma, comprises specificities, and antigen-binding domain
 PT specific to human CD19 and CD16.
 XX Example 1; SEQ ID NO 3; 38pp; English.
 XX This invention relates to a novel multivalent multimeric antibody (a
 CC bispecific diabody - BsbD) which comprises at least two binding sites
 CC specific for the human B cell marker CD19 and human Fc gamma receptor III
 CC (CD16). The invention may allow the development of compositions with
 CC cytostatic or immunosuppressive activity. The antibody is useful for the
 CC diagnosis and treatment of B-cell malignancies such as non-Hodgkin
 CC lymphoma, B-cell mediated autoimmune diseases or the depletion of B-
 CC cells. The multivalent multimeric antibody avoids the undesired immune
 CC response such as human anti-murine antibody response. The specification
 CC provides a process for stable high yield of recombinant antibodies. The
 CC present sequence is that of a mature mouse derived protein encoded by the
 CC DNA sequence of the CD19 x CD16 BsbD in the expression plasmid pSKID19x16
 CC which was used in the exemplification of the invention.
 XX SQ Sequence 272 AA;
 Query Match 83.8%; Score 1231.5; DB 7; Length 272;
 Best Local Similarity 85.7%; Pred. No. 1e-76;
 Matches 234; Conservative 14; Mismatches 22; Indels 3; Gaps 2;
 QY 3 QVQLQSGAEELARPGASVKMSCKASGYTFYTIHWVRQRPGLDLEWIGYINPSSGYS 62
 DB 1 QVQLQSGAEELARPGASVKMSCKASGYTFYTIHWVRQRPGLDLEWIGYINPSSGYS 60
 QY 63 QNQNFGKTTLTADKSSNTAYMQLNSLTSDSAVYVCARR--ADYGNVYTWFAWQGGTT 120
 DB 61 NGKFKGKATLTADSSSTAYMQLNSLTSDSAVYVCARR--ADYGNVYTWFAWQGGTT 119
 QY 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180
 DB 120 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 179
 QY 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHHVFGGTT 240
 DB 180 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHHVFGGTT 239
 QY 241 KLTVLGQPKSAAGSEQKLISEEDLNSHHHHH 273
 DB 240 KLTVLGQPKSAAGSEQKLISEEDLNSHHHHH 272
 RESULT 3
 AAR56484
 ID AAR56484 standard; protein; 415 AA.
 XX AC AAR56484;
 XX DT 25-MAR-2003 (revised)
 DT 26-MAR-1995 (first entry)
 XX SCFV pRAS109 and pRAS113.
 XX Amplification; single chain variable region fusion protein; PCR.
 XX

QY 177 KPDLFTGLTNNRPGVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWF 236
 Db 198 KPDLFTGLTNNRPGVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWF 257

QY 237 GGCTKLTVLG 246
 Db 258 GGCTKLTVLG 267

RESULT 7
 AAR22568

ID AAR22568 standard; protein; 256 AA.

XX AAR22568;

DT 21-MAY-1992 (first entry)

XX ScFvB18 construct.

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 103

FT /label= mutation
 FT /note= "Ala -> Val (VH FR3) x 3 "

FT Misc-difference 235
 FT /label= mutation

FT /note= "Tyr -> Asp (VL CDR3) x 1 "

FT Misc-difference 236
 FT /label= mutation

FT /note= "Ser -> Gly (VL CDR3) x 1 "

FT Misc-difference 242
 FT /label= mutation

FT /note= "Gly -> Ser (VL FR4) x 21; or Gly -> Asp (VL FR4) x 3 "

FT Misc-difference 245
 FT /label= mutation

FT /note= "Thr -> Ile (VL FR4) x 1 "

FT W09201047-A.

FT 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.

XX 19-OCT-1990; 90GB-00022845.

XX 12-NOV-1990; 90GB-00024503.

XX 06-MAR-1991; 91GB-00004744.

XX 15-MAY-1991; 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX N-PSDB; AAQ21100.

XX Producing members of specific binding pairs - by expression in

XX recombinant host cells with a secreting replicable genetic display

XX package.

XX Example 38; Fig 44; 209pp; English.

XX The sequence is encoded by an antibody scFv fragment directed against 4-

XX hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb against

CC NP were separately amplified and reassembled to form the construct, which
 CC was then ligated into the fd gene III contg. vector, fdcAT2, derived from
 CC fdrp/xh. (See AAQ21095). The clone having the scFvB18 sequence fused in
 CC frame to gene III was designated fdcAT2scFvB18. Alternatively the
 CC fragment was cloned into fdcOGkan (fdcAT2 with the tet gene replaced by a
 CC kanamycin resistance gene) to give fdcOGkan-scFvB18, or into the phagemid
 CC PHEN1 to create PHEN1-scFvB18. The constructs were used to test the
 CC effect of using muta- tor strains to increase the diversity of the cloned
 CC genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1:
 CC NR9046 mutT1::Tn10 were constructed by pl transduction. After 4 rounds of
 CC mutation and screening, 40 phage inserts were sequenced. They each
 CC displayed single mutations in 6 different positions, five being in the
 CC light chain region. More than 70% of the mutations occurred at positions
 CC 724 and 725 (of the nucleotide sequence) changing the first Gly in the J
 CC segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The
 CC mutant fragments had affinities for NP which were comparable to the wild-
 CC type scFv fragment (20nM). N.B. fdcAT2 is also referred to as fd-tet-DOG1
 CC and fdcOG1. See also AAR21260-307, 309-311; AAR22450, 565-581
 XX
 XX Sequence 256 AA;

Query Match 69.1%; Score 1015.5; DB 2; Length 256;
 Best Local Similarity 78.7%; Pred. No. 6.7e-62;
 Matches 200; Conservative 17; Mismatches 30; Indels 7; Gaps 3;

QY 2 AQVQLQSGAEELARPGASVKMSCKASGYTFYTIHWRQRPGRHLEWIGYINPSSGYSD 61
 Db 6 AQVQLQSGAEELVKPGASVKLSCKASGYTFISYMHVVKQRPGRGLEWIGRIDPNSGK 65

QY 62 YNQNPFGKTTLTADKSNNTAYMQLNSLTSDSAVYICARRADYGNVYTFAYKQGTTV 121
 Db 66 YNEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICA-RYDYGSSTY--FDYWGQGTTV 122

QY 122 TVSS-----AKTTPKLGDIQAVVTOESALTTSPGETVLTCSRNTGVTTSNYANWVQEK 177
 Db 123 TVSSGGGGGGGGGGGGGSAVGTFQESALTTSPGETVLTCSRSTGAVTTSNYANWVQEK 182

QY 178 PDHLFTGLTNNRPGVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWF 237
 Db 183 PDHLFTGLTNNRPGVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWF 242

QY 238 GGTKLTVLGQPKSA 251
 Db 243 GGTKLTVLEIKRAA 256

RESULT 8
 AAR22584

ID AAR22584 standard; protein; 256 AA.

XX AAR22584;

XX 21-MAY-1992 (first entry)

XX ScFvB18 construct #3.

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;

XX g3p; binding; adsorption; gene VIII; diverse repertoire;

XX specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 236

XX /label= mutation

XX /note= "Ser -> Gly (VL CDR3) "

XX W09201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

```
PR 10-JUL-1990; 90GB-00015198.
PR 19-OCT-1990; 90GB-00022845.
PR 12-NOV-1990; 90GB-00024503.
PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
PA (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
XX WPI; 1992-056862/07.
DR N-PSDB; AAQ23860.
XX
XX Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX
XX Example 38; Fig 44; 209pp; English.
XX
XX The sequence is encoded by an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb against
CC NP were separately amplified and reassembled to form the construct, which
CC was then ligated into the fd gene III contg. vector. fdCAT2, derived from
CC fdTP8/Xh. (See AAQ21095). The clone having the scFvB18 sequence fused in
CC frame to gene III was designated fdCAT2scFvB18. Alternatively the
CC fragment was cloned into fdOGkan (fdCAT2 with the tet gene replaced by a
CC kanamycin resistance gene) to give fdOGkanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test the
CC effect of using muta- tor strains to increase the diversity of the cloned
CC genes. The strains NR904mutD5: NR9046 mutD5: Tn10 and NR9046mutL:
CC NR9046 mutL::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in the
CC light chain region. More than 70% of the mutations occurred at positions
CC 724 and 725 (of the nucleotide sequence) changing the first Gly in the J
CC segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The
CC mutant shown here occurred once. The mutant fragments had affinities for
CC NP which were comparable to the wild- type scFv fragment (20nM). N.B.
CC fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1. See also AAR21260-
CC 307, 309-311; AAR22450, 565-581
XX
XX Sequence 256 AA;
SQ
Query Match 69.0%; Score 1014.5; DB 2; Length 256;
Best Local Similarity 78.7%; Pred. No. 7.9e-62;
Matches 200; Conservative 16; Mismatches 31; Indels 7; Gaps 3;
QY 2 AQVLOQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGYSD 61
DB 6 AQVLOQSGAELVKPGASVKLSCKASGYTFYSYMHVWVKQRPGRGLEWIGRIDPNSSGGT 65
QY 62 YNQNFKGKTLTADKSSNTAYMQLNSLTSEDSAVYICARRADYGNYEYTWFAYWGGTTV 121
DB 66 YNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYICAR-RYDYGSSYY--FDYWGOGTTV 122
QY 122 TVSS-----AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSYANVWQEK 177
DB 123 TVSSGGGGGGGGGGGGGQAVGTQESALTTSPGETVTLTCRSSTGAVTTSYANVWQEK 182
QY 178 PDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWFG 237
DB 183 PDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWFG 242
QY 238 GGKTLTVLGQPKSA 251
DB 243 GGKTLTVLEIKRAA 256
RESULT 9
AAR56483
ID AAR56483 standard; protein; 435 AA.
```

```
XX AAR56483;
AC
XX 25-MAR-2003 (revised)
DT 26-MAR-1995 (first entry)
XX
XX ScFv pRAS108 and pRAS112.
XX
XX Amplification; single chain variable region fusion protein; PCR.
KW
XX Synthetic.
OS
XX WO9415644-A1.
PN
XX 21-JUL-1994.
PD
XX 17-JAN-1994; 94WO-GB0000087.
PF
XX 15-JAN-1993; 93GB-00000686.
PR
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX Epenetos AA, Spooner RA, Deonarain M;
PI
XX WPI; 1994-248907/30.
DR N-PSDB; AAQ70659.
DR
XX New cpds. comprising a targetting portion and a cytotoxic portion - used
PT esp. for treating mammals for destroying target cells, partic. tumour
PT cells.
XX
XX Disclosure; Fig 9; 114pp; English.
PS
XX The sequence is that of the ScFv pRAS108 and pRAS112 between HindIII and
CC EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 435 AA;
SQ
Query Match 69.0%; Score 1014.5; DB 2; Length 435;
Best Local Similarity 74.2%; Pred. No. 1.4e-61;
Matches 201; Conservative 22; Mismatches 41; Indels 7; Gaps 2;
QY 1 MAQVLOQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGYVS 60
DB 21 MAQVLOQSGAELVKPGASVKLSCKASGYTFYSYMHVWVKQRPGRGLEWIGRIDPNSSGGT 80
QY 61 DYQNPFKGTTLTADKSSNTAYMQLNSLTSEDSAVYICARRADYGNYEYTWFAYWGGTT 120
DB 81 KYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYICAR---YDYGSSYFDYWGGTT 137
QY 121 TVSS-----AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSYANVWQEK 176
DB 138 TVSSGGGGGGGGGGGGGQAVVTQESALTTSPGETVTLTCPSSTGAVTTSYANVWQEK 197
QY 177 KPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 236
DB 198 KPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 257
QY 237 GGKTLTVLGQPKSAAGSEQKLISEDLNS 267
DB 258 GGKTLTVLGLEAPAAAPADPSKDSKAQVSA 288
RESULT 10
AAR22582
ID AAR22582 standard; protein; 256 AA.
XX
XX AAR22582;
AC
XX 21-MAY-1992 (first entry)
DT
XX ScFvB18 construct mutant #1.
DE
```


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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:28:13 ; Search time 26.5346 Seconds
(without alignments)
989.922 Million cell updates/sec

Title: US-10-049-404-3
Perfect score: 1470
Sequence: 1 MAQVQLQQSGAELARGASV.....GSEQLISBEDLNHHHHH 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.5	41.0	268	A56446	Ig heavy chain v r
2	578	39.3	287	PC4402	pelB leader/Ig hea
3	572	38.9	214	PC4156	Ig lambda chain v
4	562	38.2	113	B54256	Ig lambda-1 chain
5	558	38.0	128	S52450	Ig lambda chain v
6	556	37.8	129	L1M64E	Ig lambda-1 chain
7	551.5	37.5	112	S06818	Ig lambda chain v
8	536	36.5	113	S06819	Ig lambda chain v
9	531.5	36.2	249	S41374	single chain Fv an
10	528.5	36.0	114	S06822	Ig lambda chain v
11	527.5	35.9	474	G2MS11	Ig gamma-2b chain
12	526	35.8	106	S20654	Ig lambda chain v
13	524.5	35.7	114	S06820	Ig lambda chain v
14	520	35.4	129	L2MS35	Ig lambda-2 chain
15	515	35.0	113	S06821	Ig lambda chain v
16	506.5	34.5	139	P80024	Ig heavy chain pre
17	502	34.1	99	S14582	Ig lambda chain v
18	493.5	33.6	99	PH1089	Ig lambda chain v
19	493	33.5	140	PH1482	Ig lambda-1 chain
20	492	33.5	116	L1MSV	Ig heavy chain v r
21	492	33.5	119	S20640	Ig lambda chain v
22	491	33.4	97	PH1090	Ig lambda chain v
23	489	33.3	99	S14584	Ig lambda chain v
24	489	33.3	100	PH1088	Ig gamma chain - m
25	482	32.8	246	S38950	Ig gamma-2a chain
26	482	32.8	446	S40295	Ig heavy chain pre
27	481.5	32.8	139	A27609	PL7-6 antibody hea
28	481	32.7	117	JC2269	Ig heavy chain v r
29	480.5	32.7	128	C37267	Ig heavy chain v r

30	480	32.7	123	2	E48677	Ig heavy chain v-D
31	480	32.7	140	1	HVMSG7	Ig heavy chain pre
32	479.5	32.6	131	2	S66537	Ig heavy chain v r
33	479.5	32.6	233	2	JC5322	p53 specific singl
34	479	32.6	99	2	S14586	Ig lambda chain v
35	479	32.6	118	2	S38565	Ig heavy chain v r
36	478.5	32.6	123	2	S60067	Ig heavy chain v r
37	477	32.4	140	2	PH1489	Ig heavy chain v-D
38	474	32.2	123	2	F48677	Ig heavy chain v r
39	473	32.2	140	2	PH1498	Ig heavy chain v r
40	473	32.2	140	2	PH1484	Ig heavy chain v r
41	472	32.1	166	2	PL0012	Ig heavy chain pre
42	471	32.0	123	2	S20646	Ig heavy chain v r
43	471	32.0	135	2	PH1493	Ig heavy chain v r
44	471	32.0	140	2	PH1488	Ig heavy chain v r
45	470.5	32.0	114	2	PL0247	Ig heavy chain v r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446

R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <TAN>

A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 41.0%; Score 602.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 7.6e-35;

Matches 133; Conservative 45; Mismatches 75; Indels 25; Gaps 7;

Qy 1 MAQVQLQQSGAELARGASVMSCKASGYTFYTHVWQRPQGHLEWIGYNPSSGYS 60
Db 1 MAQVQLQESGAELVKGASVKLSCTTSGFNIKDTYHWHVWQRPQGLEWIGRIAPANGIT 60

Qy 61 DYNQNPFGKTLTADKSSNTAYMOLNSLTSEDSAVVYCARRADYGNVEYTWFA-YMGQGT 119

Db 61 KYDPKFGKATIAADTSSNTAYLQLSLTSEDTAVYICA-----SYLTRYENYWGQGT 114

Qy 120 TVTVSS-----AKTTPKLGDIQAVVTQESA-LTTPSGETVLTCSRNTGTVTTSNYANWV 174

Db 115 TVTVSSGGSGGGSGGGSDIELTQSPAIMSALGKVTMSCRSSV---NFIYVY 170

Qy 175 QEKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIFCALWYNNHW 234

Db 171 QQKSDASPKLWVYVTSHPGVPARFSGSGGSNSYLSLTSSMEGEDAATYCCQFTSPF 230

Qy 235 VFGGTHKLTIVLGQPKSNA-----AGSEQKLISEEDLN 266

Db 231 TFGSGTKLEI---KRSAAHHHHHGAABQKLISEEDLN 265

RESULT 2

PC4402

pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein

C;Species: synthetic

C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

C;Accession: PC4402

R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997

A;Title: Construction, bacterial expression, and characterization of haptten-specific si

A;Reference number: PC4402

A;Molecule type: protein
A;Residues: '2', 21-25, 'Q', 27-129 <APP>
A;Cross-references: UNIPARC:UPI0000173722
A;Accession: C93775
A;Molecule type: protein
A;Residues: 20-129 <AP2>
A;Cross-references: UNIPARC:UPI0000173722
A;Note: compositions and partial sequences of MOPC 104E
P;Casari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Reference number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
A;Accession: A93784
A;Molecule type: protein
A;Residues: 20-129 <CES>
A;Cross-references: UNIPARC:UPI0000173723
A;Accession: B93784
A;Molecule type: protein
A;Residues: 20-129 <CE2>
A;Cross-references: UNIPARC:UPI0000173723
A;Accession: C93784
A;Molecule type: protein
A;Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CE3>
A;Cross-references: UNIPARC:UPI0000173723
A;Note: these proteins were isolated from serum or urine of tumor-bearing mice
P;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
A;Accession: A90780
A;Molecule type: DNA
A;Residues: 1-43, 'T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>
A;Cross-references: UNIPARC:UPI0000270B5
A;Note: the sequence was determined from the differentiated gene
P;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
A;Accession: C93282
A;Molecule type: DNA
A;Residues: 1-58, 'E', 60-89, 'D', 91-98, 'T', 100-105, 'W', 107-129 <BOT>
A;Cross-references: UNIPARC:UPI00000270B7
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.
C;Genetics:
A;Introns: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglytamic acid
P;1-19/Domain: signal sequence #status experimental <SIG>
P;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>
P;34-111/Domain: immunoglobulin homology <IMM>
P;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
P;41-109/Disulfide bonds: #status predicted

Query Match 37.8%; Score 556; DB 1; Length 129;
Best Local Similarity 92.1%; Pred. No. 5.6e-32;
Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 133 GGDQAVVQBSALTTSPGETVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNR 192
Db 16 GAISQAVVQBSALTTSPGETVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNR 75

Qy 193 APGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246
Db 76 APGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

RESULT 7

S06818
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06818
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06818
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-112 <MIL>
A;Cross-references: UNIPARC:UPI000017683F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 37.5%; Score 551.5; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 9.8e-32;
Matches 105; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 138 AVVTQESA-LTTSPEGTVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNRPGV 196
Db 1 AVVTQESALTTSPGETVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNRPGV 60

Qy 197 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLGQP 248
Db 61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLGQP 112

RESULT 8
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06819
A;Molecule type: mRNA
A;Residues: 1-113 <MIL>
A;Cross-references: UNIPARC:UPI0000115E3C; EMBL:X17168; NID:G52251; PIDN:CAA35046.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

Query Match 36.5%; Score 536; DB 2; Length 113;
Best Local Similarity 94.4%; Pred. No. 1.2e-30;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 138 AVVTQESALTTSPGETVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNRPGV 197
Db 1 AVVTQESALTTSPGETVTLTCRSNTGVTTSNYANWVQSKPDHLFTGLIGHTNNRPGV 60

Qy 198 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVL 245
Db 61 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVL 108

RESULT 9
S41374
single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antib
A;Reference number: S41374


```
Db 19 SEVLOQSGPELVNPGASVVMKSCASGYFTITYVMHVVWKQPKQGLEWIGYINPNKDGTK 78
Qy 62 YNQNFKGTWLTADKSNNTAYMOLNSLTSDSAVYTCARRADYGNVYTWFAVWGQGTTV 121
Db 79 FNEKPKGKATLTSKSNNTAYMELUSSLTSDSAVYTCAR-----DYDYDFAFVWGQGTTLV 133
Qy 122 TVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCRSNTGTVTTS 168
Db 134 TVSAAKTTP-----PSVYPLAPG-----CGDRTGSSVTS 162

RESULT 12
S20654
Ig lambda chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S20654
R/Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A/Reference number: S20639
A/Accession: S20654
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-106 <LOS>
A/Cross-references: UNIPARC:UPI0000116029; EMBL:X65012; NID:G52705; PIDN:CAA46145.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 526; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 5.4e-30;
Matches 99; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 137 QAVVTOESALTTSPGETVTLTCRSNTGTVTTSNVANVQEKPDHLFTGLIGHTNNRPGV 196
Db 1 QAVVTOESALTTSPGETVTLTCRSIGAVTTSNAYVQEKPDHLFTGLIGTNNRPGV 60
Qy 197 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKL 242
Db 61 PVRFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKL 106

RESULT 13
S06820
Ig lambda chain V region (clone 12B4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C/Accession: S06820
R/Miller III, A.; Glaeser, J.A.
J. Mol. Biol. 209, 763-778, 1989
A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A/Reference number: S06815; MUID:90064531; PMID:2555519
A/Accession: S06820
A/Molecule type: mRNA
A/Residues: 1-114 <MIL>
A/Cross-references: UNIPARC:UPI0000176812; EMBL:X17169
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>
F:22-90/Disulfide bonds: #status predicted

Query Match 35.7%; Score 524.5; DB 2; Length 114;
Best Local Similarity 93.6%; Pred. No. 7.4e-30;
Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 138 AVVTOES-ALTTSPGETVTLTCRSNTGTVTTSNVANVQEKPDHLFTGLIGHTNNRPGV 196
Db 1 AVVTOESIXLTTSPGETVTLTCRSNTGAVTTSNVANVQEKPDHLFTGLIGTNNRPGV 60
Qy 197 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKLTVL 245
Db 61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKLTVL 109
```

RESULT 14

L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1980 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C/Accession: A93431; B93282; B91462; A90372; A90410; S09391; A01997

R/Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.

Nucleic Acids Res. 10, 3831-3843, 1982

A/Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene

A/Reference number: A93431; MUID:82274221; PMID:6287422

A/Accession: A93431

A/Molecule type: mRNA

A/Residues: 1-129 <WUG>

A/Cross-references: UNIPROT:P01729; UNIPARC:UPI00000270BD

R/Bothwell, A.L.M.; Paikind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,

Nature 298, 380-382, 1982

A/Title: Somatic variants of murine immunoglobulin lambda light chains.

A/Reference number: A93282; MUID:82220143; PMID:6283385

A/Accession: B93282

A/Molecule type: DNA

A/Residues: 1-129 <BOT>

A/Cross-references: UNIPARC:UPI00000270BD

A/Note: the sequence was determined from the differentiated gene

R/Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.

Fed. Proc. 38, 1839-1845, 1979

A/Title: Structure and function of immunoglobulin genes and precursors.

A/Reference number: A91462; MUID:79148758; PMID:428562

A/Accession: B91462

A/Molecule type: protein

A/Residues: 1-22 <SCH>

A/Cross-references: UNIPARC:UPI0000173724

R/Dugan, E.S.; Bradehaw, R.A.; Simms, E.S.; Eisen, H.N.

Biochemistry 12, 5400-5416, 1973

A/Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).

A/Reference number: A90372; MUID:74048693; PMID:4760498

A/Accession: A90372

A/Molecule type: protein

A/Residues: 20-24, 'E', 26-73, 'D', 75-129 <DUG>

A/Cross-references: UNIPARC:UPI0000173725

R/Gavish, M.; Zakut, R.; Wilchek, M.; Givol, D.

Biochemistry 17, 1345-1351, 1978

A/Title: Preparation of a semisynthetic antibody.

A/Reference number: A90410; MUID:78187254; PMID:418802

A/Accession: A90410

A/Molecule type: protein

A/Residues: 1-129 <GAV>

A/Cross-references: UNIPARC:UPI00000270BD

R/Bogen, B.; Lambris, J.D.

EMBO J. 8, 1947-1952, 1989

A/Title: Minimum length of an idiotype peptide and a model for its binding to a major

A/Reference number: S09391; MUID:90005397; PMID:2792076

A/Accession: S09391

A/Molecule type: protein

A/Residues: 110-126 <BOG>

A/Cross-references: UNIPARC:UPI0000173726

C/Comment: This chain is from a myeloma protein with anti-DNP activity.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; pyroglutamic acid

F:1-19/Domain: signal sequence #status experimental <SIG>

F:20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>

F:34-111/Domain: immunoglobulin homology <IMM>

F:110-126/Region: idiotype to histocompatibility complex class II #status experimental

F:210/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim

F:41-109/Disulfide bonds: #status predicted

Query Match 35.4%; Score 520; DB 1; Length 129;

Best Local Similarity 85.1%; Pred. No. 1.8e-29;

Matches 97; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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QY 133 GGDIAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWVQEKPDHLFTGLIGHTNNR 192
Db 16 GASSQAVVTQESALTTSPGGTVLTCRSSTGAVTTSNYANWIOEKPDHLFTGLIGTSNR 75
QY 193 APOVPAFPQSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246
Db 76 APOVPAFPQSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

RESULT 15
S06821
Ig lambda chain V region (clone 11C7) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C:Accession: S06821
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morph
A:Reference number: S06815; MUID:90064531; PMID:2555519
A:Accession: S06821
A:Molecule type: mRNA
A:Residues: 1-113 <MIL>
A:Cross-references: UNIPARC:UPI000115E3E; EMBL:X17170; NID:G52253; PIDN:CAA35048.1; PID
A>Note: the authors translated the codon AGT for residue 47 as Gly, GTT for residue 56 a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer, immunoglobulin
F:14-91/Domain: immunoglobulin homology <IMM>
F:21-89/Disulfide bonds: #status predicted

Query Match 35.0%; Score 515; DB 2; Length 113;
Best Local Similarity 86.6%; Pred. No. 3.4e-29;
Matches 97; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 138 AVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWVQEKPDHLFTGLIGHTNNRAPGVP 197
Db 1 AVVTQESILTTSPGETVTLTCRSSTGAVTTSNYANWVQKPDHLFTSLIGISNRVPGVP 60
QY 198 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLGQPK 249
Db 61 ARFSGSLIGDKVALTITGTQTEDEAIYFCALWYNNHWVFGGKTLTVLQPE 112
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Search completed: February 9, 2006, 03:34:19
Job time : 27.5346 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: February 9, 2006, 03:18:36 ; Search time 167.882 Seconds
(without alignments)
1147.288 Million cell updates/sec
Title: US-10-049-404-3
Perfect score: 1470
Sequence: 1 MAQVQLQSGAEELARPGASV.....GSEQKLISEEDLNHHHHH 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	40.6	243	2	Q7TQM2 mus musculus
2	590	40.1	487	2	Q65ZL2_MOUSE
3	559	38.0	129	1	LVID_MOUSE
4	557	37.9	129	1	LVIE_MOUSE
5	556	37.8	129	1	LVIB_MOUSE
6	555	37.8	110	1	LVIC_MOUSE
7	548.5	37.3	113	2	Q8CGS1_MOUSE
8	545	37.1	129	2	Q8VDE2_MOUSE
9	539	36.7	255	2	Q6KB05_MOUSE
10	538.5	36.6	109	2	Q9ET13_MOUSE
11	533	36.3	244	2	Q65ZC8_HUMAN
12	520	35.4	129	1	LV2B_MOUSE
13	519.5	35.3	473	2	Q8D81A_MOUSE
14	512.5	34.9	617	2	Q4KML5_MOUSE
15	510	34.7	241	2	Q921A6_MOUSE
16	499	33.6	468	2	Q569W9_MOUSE
17	494.5	33.6	117	1	LV1A_MOUSE
18	490	33.3	120	1	HV03_MOUSE
19	487	33.1	240	2	Q65ZC9_HUMAN
20	481	32.7	472	2	Q6FJA7_MOUSE
21	480	32.7	140	1	HV02_MOUSE
22	479.5	32.6	463	2	Q99LC4_MOUSE
23	479	32.6	616	2	Q504M7_MOUSE
24	478.5	32.6	465	2	Q8PJB2_MOUSE
25	476	32.4	470	2	Q7EMK1_MOUSE
26	472	32.1	168	2	Q8VDC9_MOUSE
27	472	32.1	458	2	Q5BJZ2_RAT
28	469.5	31.9	613	2	Q8VCX7_MOUSE
29	468.5	31.9	489	2	Q8VCX4_MOUSE
30	466.5	31.7	139	1	HV07_MOUSE
31	466	31.7	134	2	Q65ZRC_MOUSE

32	465.5	31.7	145	2	Q924Q7_MOUSE	Q924q7 mus musculus
33	463.5	31.5	142	2	Q924Q1_MOUSE	Q924q1 mus musculus
34	463.5	31.5	146	2	Q924Q3_MOUSE	Q924q3 mus musculus
35	463.5	31.5	146	2	Q924R8_MOUSE	Q924r8 mus musculus
36	463	31.5	482	2	Q8K172_MOUSE	Q8k172 mus musculus
37	462	31.4	117	1	LV2A_MOUSE	P01728 mus musculus
38	461	31.4	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculus
39	461	31.4	143	2	Q924R7_MOUSE	Q924r7 mus musculus
40	461	31.4	145	2	Q924R4_MOUSE	Q924r4 mus musculus
41	459.5	31.3	248	2	Q65ZQ7_MOUSE	Q65zq7 mus sp. b3
42	459.5	31.3	590	2	Q4V9V8_MOUSE	Q4v9v8 mus musculus
43	459	31.2	143	2	Q924Q5_MOUSE	Q924q5 mus musculus
44	457.5	31.1	477	2	Q58E56_MOUSE	Q58e56 mus musculus
45	457	31.1	138	1	HV49_MOUSE	P03980 mus musculus

ALIGNMENTS

RESULT 1

ID Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ScFv 6H8 protein (Fragment).
GN Name-scfv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor";
RL J. Biol. Chem. 278:36740-36747(2003).
RL EMBL; AJ574851; CAB00495.1; -; Genomic_DNA.
DR HSP; P01751; 1A6W.
DR SMR; Q7TQM2; 1-236.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFFP6D2DCF4F76 CRC64;

Query Match 40.6%; Score 597; DB 2; Length 243;
Best Local Similarity 47.3%; Pred. No. 2.6e-39;
Matches 131; Conservative 29; Mismatches 77; Indels 40; Gaps 6;

Qy	3	QVQLQSGAEELARPGASVKMSCKASGYTFYTHHWQRPGHLEWIGYINPSSGSDY	62
Db	1	QVQLQSGSELRPGASVKLSCKASGYTFYTHHWKQRHGQGLEWIGNYPGSGITNY	60
Qy	63	QNQFKGKTTLTADKSSNTAYMQLNSLTSEDSAVVYCCARRADYGNVYTFWFGQGT	122
Db	61	DEKFNKGILLTVDTSSTAYMHLSSLASEDSAVVYCCARRADYGNVYTFWFGQGT	113
Qy	123	VSSAKTPPKLGG-----DIQAVTQSSALTSGETVTLPCRSTGTVTISNYANWQE	176
Db	114	VSSGGGGGGGGGGGGSDIQ-MTQSSSFVSLGDRVTITCKASEDIY---NRLAWQQ	169
Qy	177	KPDHLFTCLIGHTNRPAGVPARFPGSLIGDKAALTITGAQTEDEAIFYFCALWYNNHW	236
Db	170	KPGNAPRLILSGATSLGTGVPFRFSGSGSGDKDYLSITSLQTEDVATVYCCQYWSTR	228
Qy	237	GGGTKLTVLGQPKSAAGSEQLISEEDLNHHHHH	273

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Db      229 GGCTKLEI-----KHHHHH 243

RESULT 2
Q65ZL2 9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN-<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
   antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 40.1%; Score 590; DB 2; Length 487;
Best Local Similarity 49.4%; Pred. No. 2.2e-38;
Matches 126; Conservative 37; Mismatches 72; Indels 20; Gaps 5;

QY 2 AQVQLQSGAEARPGASVKMSCKASGYTFTYTHWVRQPGHDLIEWIGYNPSSGYS 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 SQVQLQSDAELVKPGASVKISCKASGYTFTDTHAIHWKQPGQLEWIGYISPGNDIK 78
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 YNQPFKGTITLADKSSNTAYMQLNSLTSEDSAVYVCARRADYGVYTFWFAWGQTTV 121
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 YNEKFGKATLTADKSSNTAYMQLNSLTSEDSAVYFCR-----SYIGHWGQTT 129
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 TVSSAKTT---PKLGGDIOAVVTOESA-LTTSPTGTTLTCRSTGTGTTTSNYAN--WVQ 175
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 TSGSGGSGSGSGSGSGSGRIQMTQSPASLSVSVELVITTCRASENI-----YSNLA 184
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 EKPDLHLFTGLIGHTNNRPGVPARFSGSLIGDKAALITGAQTEDEAIFYCALWYNNHW 235
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 QKQKSPQLLVYAATNLADGVPRFSGSGSGTQYSLKINSLSQEDFGSYCYCHFWCTPT 244
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 FGGGKTLVIGQPKS 250
Db 245 FGGGTRLEIKPRSKS 259

RESULT 3
LVIE_MOUSE STANDARD; PRT; 129 AA.
AC P01726;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 01, Last annotation update)
DE Ig lambda-1 chain V region H2020 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
   Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use.
```

CC use as long as its content is in no way modified and this statement is not
CC removed.

CC HSSP; P01724; 1A6V.
CC SNR; P01727; 20-129.
CC Ensembl; ENSMUSG00000064012; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; P050835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 129 Ig lambda-1 chain V region S43.
FT DOMAIN 20 125 Ig-like.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 13529 MW; 84E54EDDD5791345 CRC64;

Query Match 37.9%; Score 557; DB 1; Length 129;
Best Local Similarity 92.1%; Pred. No. 1.8e-36;
Matches 105; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 GGDIAVVTQESALTTSPGETVTLTCSRNTGTTTSNYANWVQKDPDHLFTGLIGTNNR 192

Db 16 GAISQAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQKDPDHLFTGLIGTNNR 75

QY 193 ARGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246

Db 76 APGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

RESULT 5

LV1B_MOUSE STANDARD; PRT; 129 AA.
AC P01724;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

PROTEIN SEQUENCE OF 1-29 (MOPC 104E), AND SEQUENCE REVISION TO 20 AND 26.

MEDLINE=77148916; PubMed=403522;
Burststein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).

[2]
PROTEIN SEQUENCE OF 20-129 (MOPC 104E AND RPC 20).
MEDLINE=71107854; PubMed=5276767;

RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).

[3]
PROTEIN SEQUENCE OF 20-129 (J558 AND S104).
MEDLINE=73229669; PubMed=4516208;

RA Cesari I.M., Weigert M.;
RT "Mouse lambda-chain sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).

CC -1- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show
CC no differences from MOPC 104E. The sequences of J558 and S104
CC seems identical with that shown.

CC -1- MISCELLANEOUS: These proteins were isolated from serum or urine of
CC tumor-bearing mice.

CC -1- MISCELLANEOUS: The MOPC 104E precursor was synthesized in a cell-
CC free system directed by mRNA isolated from MOPC 104E myeloma
CC polysomes. Met-1 was lacking in 90% of the chains. It is probably
CC rapidly cleaved after synthesis.

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR; B93815; L1MS4E.

DR PDB; 1A6U; X-ray; L=21-128.

DR PDB; 1A6V; X-ray; L/M=N=20-128.

DR PDB; 1A6W; X-ray; L=21-128.

DR Ensembl; ENSMUSG00000064012; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; P050835; IG_LIKE; 1.

KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.

FT SIGNAL 1 19

FT CHAIN 20 129 Ig lambda-1 chain V regions MOPC

104E/RPC20/J558/S104.

FT DOMAIN 20 125

FT MOD_RES 20 20

FT NON_TER 129 129

FT STRAND 23 25

FT STRAND 28 31

FT TURN 33 34

FT STRAND 36 43

FT TURN 44 45

FT STRAND 46 46

FT HELIX 50 52

FT STRAND 55 60

FT TURN 61 63

FT STRAND 64 70

FT TURN 71 73

FT STRAND 74 75

FT TURN 77 78

FT TURN 81 82

FT STRAND 83 88

FT TURN 89 90

FT STRAND 91 97

FT HELIX 101 103

FT STRAND 105 112

FT STRAND 117 119

FT STRAND 123 127

FT SEQUENCE 129 AA; 13479 MW; 03629939D5791AC0 CRC64;

Query Match 37.8%; Score 556; DB 1; Length 129;

Best Local Similarity 92.1%; Pred. No. 2.1e-36;

Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 133 GGDIAVVTQESALTTSPGETVTLTCSRNTGTTTSNYANWVQKDPDHLFTGLIGTNNR 192

Db 16 GAISQAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQKDPDHLFTGLIGTNNR 75

QY 193 ARGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246

Db 76 APGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

RESULT 6

LV1C_MOUSE STANDARD; PRT; 110 AA.

AC P01725;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig lambda-1 chain V region S178.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
PROTEIN SEQUENCE.
RX MEDLINE=73229669; PubMed=4516208;
RA Cesari I.M., Weigert M.;
RT "Mouse lambda-chain sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
CC -I- MISCELLANEOUS: This protein was isolated from serum or urine of
CC tumor-bearing mice.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01724; 1A6V.
DR SMR; P01725; 1-110.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 106
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11654 MW; 7D06718E1A530206 CRC64;

Query Match 37.8%; Score 555; DB 1; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-36;
Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 137 QAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWQKPDHLFTGLIGHTNNRPGV 196
Db 1 QAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWQKPDHLFTGLIGHTNNRPGV 60

OY 197 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 246
Db 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 110

RESULT 7
Q8CGS1 MOUSE
ID Q8CGS1_MOUSE PRELIMINARY; PRT; 113 AA.
AC Q8CGS1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-deoxynivalenol scFv lambda light chain variable region
DE (Fragment).
GN Names=Igl-V1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=BALB/c;
RC Ensembl; ENSMUSG0000064012; Mus musculus.
RA Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV151141; AAN75453.1; -; mRNA.
DR HSSP; P01724; 1A6V.
DR SMR; Q8CGS1; 1-113.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR MGI; MGI:96530; Igl-V1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT DOMAIN 1 106
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11654 MW; 7D06718E1A530206 CRC64;

Query Match 37.8%; Score 545; DB 2; Length 129;
Best Local Similarity 90.4%; Pred. No. 1.6e-35;
Matches 103; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 133 GGDIOAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWQKPDHLFTGLIGHTNNR 192
Db 16 GAISQAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWQKPDYLTGLIGGTTNR 75

OY 193 AFGVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 246
Db 76 AFGVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 129

RESULT 8
Q8VDE2 MOUSE
ID Q8VDE2_MOUSE PRELIMINARY; PRT; 129 AA.
AC Q8VDE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin lambda chain variable region (Fragment).
GN Name=Igl-V1; Synonyms=4G12-A-H10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC Ensembl; ENSMUSG0000064012; Mus musculus.
RA Melle G.;
RL Thesis (1995), Department of Ecole Supérieure de Technicien en
RL Biologie Biochimie, Université Catholique de Lyon, Lyon, France.
RN [2]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC Ensembl; ENSMUSG0000064012; Mus musculus.
RA Blachere T.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ291694; CAC82790.1; -; mRNA.
DR HSSP; P01724; 1A6V.
DR SMR; Q8VDE2; 20-129.
DR MGI; MGI:96530; Igl-V1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13565 MW; C07F71003803ADBE CRC64;

Query Match 37.1%; Score 545; DB 2; Length 129;
Best Local Similarity 90.4%; Pred. No. 1.6e-35;
Matches 103; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 133 GGDIOAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWQKPDHLFTGLIGHTNNR 192
Db 16 GAISQAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWQKPDYLTGLIGGTTNR 75

OY 193 AFGVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 246
Db 76 AFGVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHVVFGGTKLTVLG 129

RESULT 9
Q6KB05 MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE SCFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
SQ
Query Match 36.7%; Score 539; DB 2; Length 255;
Best Local Similarity 41.3%; Pred. No. 1.1e-34;
Matches 116; Conservative 39; Mismatches 90; Indels 36; Gaps 6;
QY 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHWVRQRPGLDLEWIGINPSSGSDY 62
DB 1 QVQLQSGDLVIRPGSLKVSCKASGFTFSYSGMSVWRQTPDKRLKLEWVITSGGSYTY 60
QY 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVYCCARRADYGNIEYTW-FAYWGQSTV 121
DB 61 PDSVKGFTISRDNKNTLYLQSSLSKSEDTAMYICARHI--NYRYDGAFDYWGQSTL 117
QY 122 TVSSAKTTPKLG-----DIQAVVQESALTTPSGETVTLTCSRNTGTWTT---SNYAN 172
DB 118 TVSSGGGGSGGGSGGGSDI-VNAQSPSSLSVSAAGEKVMSCSKSOSLLNSRNQKNYLA 176
QY 173 WVEKPHLFTGLIHTNNRAGVPAPRPSGLIGDKAALITGAQTDEAIYFCALWYNN 232
DB 177 WYQQKPGQSPKLLIYGASTRESGVDRFTGSGSGTDFTLTSSVQASDLAVIYQNDHSY 236
QY 233 HWVFGGTTKLVLGQPKSAAGSEKLSISERDLNSHHHHH 273
DB 237 PLTFGAGTKLEI-----KHHHHH 255
RESULT 10
Q9ET13_MOUSE PRELIMINARY; PRT; 109 AA.
AC Q9ET13;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Song M.-Y., Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF287275; AAG03053.1; -; mRNA.
DR HSSP; P01724; 1A6V.
DR SMR; Q9ET13; 1-109.
DR Ensembl; ENSMUSG00000064012; Mus musculus.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 11554 MW; 4F91E9D351B1E158 CRC64;
SQ
Query Match 36.6%; Score 538.5; DB 2; Length 109;
Best Local Similarity 92.7%; Pred. No. 4.3e-35;
Matches 102; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY 137 QAVVQESALTTPSGETVTLTCSRNTGTWTTSNYANWVQEKPHLFTGLIHTNNRAGV 196
DB 1 QAVVQESALTTPSGETVTLTCSRSTGAIITNNFANWVQEKPHLFTGLIHTNNRPGV 60
QY 197 PARFSGSLIGDKAALITGAQTDEAIYFCALWYNNHVVFGGTTKLVLG 246
DB 61 PARFSGSLIGDKAALITGAQTDEAIYFCALWYNN-VWFGGTTKLVLG 109
RESULT 11
Q6SZC8_HUMAN PRELIMINARY; PRT; 244 AA.
ID Q6SZC8_HUMAN PRELIMINARY;
AC Q6SZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbr0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
FT SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
SQ
Query Match 36.3%; Score 533; DB 2; Length 244;
Best Local Similarity 46.6%; Pred. No. 3.2e-34;
Matches 118; Conservative 39; Mismatches 74; Indels 22; Gaps 6;
QY 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHWVRQRPGLDLEWIGINPSSGSDY 62
DB 1 QVQLQSGAEVKKPDSVKVSKASGYTFSDHYHWHWRQAPGQGLEWGWIDPNNGDRF 60
QY 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVYCCARR-----ADYGNIEYTWYWGQ 118
DB 61 AQRFGRTWTRDTISAAIYEVSRSLSDDTAVIYCAREGTGSAIY-----MDVWQGG 114
QY 119 TTVTVSSAKTTPKLG-----DIQAVVQESALTTPSGETVTLTCSRNTGTWTTSNYA 171
DB 115 TLTVTVSSGGGGSGGGSGGGSDIQ--MTQSPFSLASIGDRVTITCSASEIY---HWL 169
QY 172 NWVEKPHLFTGLIHTNNRAGVPAPRPSGLIGDKAALITGAQTDEAIYFCALWYNN 231
DB 170 AWYQQKPKGAPKFLIYKASSLASGAPSRFSGSGSGTDFTLTSSLPDPPATYIYQQYSN 229
QY 232 NHWVFGGTTKLV 244
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Db 230 YPLTFGGGKLEI 242
|||||
20 129 1g lambda-2 chain V region MOPC 315.
FT CHAIN 20 129 1g-like.
FT DOMAIN 20 125 Pyrrolidone carboxylic acid.
FT MOD_RES 20 20
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13418 MW; 0AA6E8125723552C CRC64;

Query Match 35.4%; Score 520; DB 1; Length 129;
Best Local Similarity 85.1%; Pred. No. 1.6e-33;
Matches 97; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY 133 GGDIAQVVTQESALTTSPGETVLTTCRSNTGTGTTTSNTYANWVQKPDHLFTGLTGHTNNR 192
Db 16 GASSQAVVTQESALTTSPGTVLTTCRSSTGAVTTSYANWVQKPDHLFTGLTGTSNR 75
OY 193 AGPVPARFSGSLIGDKAALITGAOTDEAIYFCALWNHNVFGGKLTVLG 246
Db 76 APGVPRFSGSLIGDKAALITGAOTDEDDAMVFCALWFRNHFVFGGKTVTLG 129

RESULT 13
Q9D8L4 MOUSE
ID Q9D8L4 MOUSE PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:181006009 product:immunoglobulin heavy chain 6 (heavy
DE chain of IGM), full insert sequence.
GN Name=Igh-la;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
```

RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK007918; BAB25349.1; -; mRNA.
DR PIR; PH1165; PH1165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.
DR HSP; P01864; IBOG.
DR SWR; Q9DBL4; 20-469.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0003033; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0005078; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
QY SEQUENCE 473 AA; 9DEDS7A514475FBB CRC64;
QY 2 AQVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIGYINPSSGYSD 61

Query Match 34.9%; Score 512.5; DB 2; Length 617;
Best Local Similarity 45.0%; Pred. No. 4.3e-32;
Matches 126; Conservative 36; Mismatches 79; Indels 39; Gaps 10;
QY 2 AQVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIGYINPSSGYSD 61

Query Match 34.9%; Score 512.5; DB 2; Length 617;
Best Local Similarity 45.0%; Pred. No. 4.3e-32;
Matches 126; Conservative 36; Mismatches 79; Indels 39; Gaps 10;
QY 2 AQVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIGYINPSSGYSD 61

Query Match 35.3%; Score 519.5; DB 2; Length 473;
Best Local Similarity 58.6%; Pred. No. 8.5e-33;
Matches 112; Conservative 20; Mismatches 40; Indels 19; Gaps 4;
QY 3 QVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIGYINPSSGYSD 62
DB 20 QVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIGYINPSSGYSD 79
QY 63 NQNFQKTKTLTADKSNATYMQNLSTSDSAVYVCARRADYCNVEYTFYAWGQGTFTVT 122
DB 80 NEKFKGKATLTADKSNATYMQNLSTSDSAVYFCAR-----SGYDYDFAYWGQGTFTVT 135
QY 123 VSSAKTT-----PKLGGDIQAVVVTQESALTSPGETVTLTCSRNTGTVTSYANWV 174
DB 136 VSAAKTTPSVVPLAPVCGTGTSSVTLGLVKGYPPVPTLTW---NSGSLSSG-----V 188
QY 175 QSKPDLHFTGL 185
DB 189 HTFPALLOSGL 199

RESULT 14
Q4KML5 MOUSE
ID Q4KML5 MOUSE PRELIMINARY; PRT; 617 AA.
AC Q4KML5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC098504; AAH98504.1; -; mRNA.
DR KW Hypothetical protein.
QY SEQUENCE 617 AA; BCF2AEC857CD3D12 CRC64;

Db 19 SQVLQOQSAGAEALAKPGASVKLSCKASGYTFSTSWMHVVKORPCQGLEWIGYNPSSGYTK 78
QY 62 YNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYYCARRADYGNIEYTFWYFWGQGTTV 121
Db 79 YNQKPKDKATLTADKSSNTAYMQLNSLTSEDSAVYYCARREGHLLWVYA-MDYWGQGTSV 137
QY 122 TVSS-AKTPKLGDDIQAVVQBSALTPSPGETVTLTCSRNGTGTVTTSYANWVQEKPDH 180
Db 138 TVSSSQSFPF---NVFPLVSCSPF--SDKNLVAMGLCLARDPLPSTISF-TWNYQNNTTE 190
QY 181 LFTGLIGHTNNRAPGVPARFSGSLIGDKAALITGAQTEDAIYFCALAYNNHNVFGGCT 240
Db 191 VIQGIKTFPLRTGGKYLATSVLLSPKSL-----EGSDEYL-VCKIHY-----GGKN 238
QY 241 K-----LTVLGOPK---SAAAGSEQKLISE 262
Db 239 KDLHVPPIPAVAENPNVNVFVPRDGFSGPAPRKSKLICE 278

RESULT 15
Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6_MOUSE (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; IBLW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 34.7%; Score 510; DB 2; Length 241;
Best Local Similarity 44.1%; Pred. No. 2.1e-32;
Matches 113; Conservative 43; Mismatches 64; Indels 36; Gaps 9;
QY 3 QVQLQOQSAGAEALAKPGASVKLSCKASGYTFSTSWMHVVKORPCQGLEWIGYNPSSGYSDY 62
Db 1 QVQLQOQSAGAEALAKPGASVKLSCKASGYTFSTSWMHVVKORPCQGLEWIGYNPSSGYSDY 60
QY 63 QNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYYCARRADYGNIEYTFWYFWGQGTTVT 122

Db 61 ADDFKGRFAFSLTSSASTAYLQINNLKNEEDTATYFCARK-DLLRY-----FDYWGQGTTVT 115
QY 123 VSSAKTTPKLG-----DIQAVVQBSALTPSPGETVTLTCSRNGTGTVTTSYANWVQ 175
Db 116 VSSGGGGSGGGGGGGSDIE--LTQSPSSLSASLGGKVTITCKASQ---DINKYIAWYQ 170
QY 176 EKPD-----HLFTGLIGHTNNRAPGVPARFSGSLIGDKAALITGAQTEDEAIYFC 226
Db 171 HKPGKGRPSAHTLHIYI-----QPGIPSRFSGSGSGDRYFSISNLEPEDATATYYC 221
QY 227 ALWYNNHNVFGGCTKL 242
Db 222 -LHYDNLHTFTGGGTKL 236
Search completed: February 9, 2006, 03:33:22
Job time : 167.882 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	1037.5	70.6	402	1	US-08-491-988-9
2	1035.5	70.4	415	1	US-08-491-988-7
3	1035.5	70.4	435	1	US-08-491-988-5
4	1026.5	69.8	269	1	US-08-428-257A-72
5	1026.5	69.8	269	1	US-08-491-988-3
6	730	49.7	288	2	US-09-423-439-38
7	696	47.3	495	2	US-09-948-004-18
8	685	46.6	258	2	US-09-526-738A-4
9	678	46.1	239	2	US-08-279-772A-8
10	678	46.1	239	2	US-08-902-486-11
11	677	46.1	246	1	US-08-469-486-57
12	677	46.1	246	1	US-08-469-658-57
13	676	46.0	256	2	US-09-526-738A-2
14	675	45.9	599	1	US-08-463-163-3
15	659.5	44.9	244	1	US-08-553-497A-20
16	657	44.7	273	1	US-08-403-853-18
17	654.5	44.5	246	1	US-08-553-497A-24
18	650.5	44.3	673	2	US-09-423-439-32
19	648	44.1	270	2	US-09-576-118-2
20	644.5	43.8	264	2	US-10-114-716A-46
21	641.5	43.6	244	1	US-08-553-497A-22
22	634	43.1	267	2	US-09-419-788-30
23	634	43.1	553	1	US-08-661-052-16
24	634	43.1	553	2	US-09-188-082-16
25	634	43.1	553	2	US-09-364-088-16
26	634	43.1	553	2	US-09-102-716-16
27	631.5	43.0	442	1	US-08-553-497A-26


```

US-08-428-257A-72
; Sequence 72, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/428,257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-257A-72

Query Match 69.8%; Score 1026.5; DB 1; Length 269;
Best Local Similarity 79.6%; Pred. No. 1.9e-69;
Matches 199; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

Qy 1 MAQVQLQDSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLSEWIGINPSSGYS 60
Db 21 MAQVQLQDSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLSEWIGRIDPNSGGT 80

Qy 61 DYNQNFKGTLLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNVYTFWYFAGQGT 120
Db 81 KYNEKFKSKATLVDPSSSTAYMQLSSLTSEDSAVVYCAR---YDYGSSYFDYWGQGT 137

Qy 121 VTSS-----AKTTPKLGDIQAVVTOESALTTSPGETVTLTCSRNTGVTTSNYANWVQ 176
Db 138 VTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 197

Qy 177 KPDLFTGLTGNRRAPGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 236
Db 198 KPDLFTGLTGNRRAPGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 257

Qy 237 GGGTKLTVLG 246
Db 258 GGGTKLTVLG 267

RESULT 5
US-08-491-988-3
; Sequence 3, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCANULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA

US-08-428-257A-72
; Sequence 72, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/428,257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-257A-72

Query Match 69.8%; Score 1026.5; DB 1; Length 269;
Best Local Similarity 79.6%; Pred. No. 1.9e-69;
Matches 199; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

Qy 1 MAQVQLQDSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLSEWIGINPSSGYS 60
Db 21 MAQVQLQDSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLSEWIGRIDPNSGGT 80

Qy 61 DYNQNFKGTLLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNVYTFWYFAGQGT 120
Db 81 KYNEKFKSKATLVDPSSSTAYMQLSSLTSEDSAVVYCAR---YDYGSSYFDYWGQGT 137

Qy 121 VTSS-----AKTTPKLGDIQAVVTOESALTTSPGETVTLTCSRNTGVTTSNYANWVQ 176
Db 138 VTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 197

Qy 177 KPDLFTGLTGNRRAPGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 236
Db 198 KPDLFTGLTGNRRAPGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 257

Qy 237 GGGTKLTVLG 246
Db 258 GGGTKLTVLG 267

RESULT 5
US-08-491-988-3
; Sequence 3, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCANULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA

```

```
;
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB98/01294
;   FILING DATE: 05-MAY-1998
;   APPLICATION NUMBER: GB 9709421.3
;   FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 38:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 288 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match      49.7%; Score 730; DB 2; Length 288;
Best Local Similarity 56.2%; Pred. No. 3.4e-47;
Matches 158; Conservative 24; Mismatches 77; Indels 22; Gaps 7;

QY 1 MAQVLOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 60
Db 21 MAQVLOQSGAELVKEGASVQLSCASGYFTFTGYWHVWVKRPGQGLEWIGVNPSTGRS 80
QY 61 DYNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGQTT 120
Db 81 DYNEKFNKATLTVDKSSSTAYMQLSLTSEDSAVYICARAYG-YDDA-MDYWGQGT 138
QY 121 VTSSAKTTPKLG-----DIQAVVTQBSALTSPGETVTLTCSRNTGTV---TTSNYA 171
Db 139 VTSSGGGGGGGGGGGGGSDIE-LSQSPSSLAVSAGEKVTWMSCKSSQSLNSTRKNYL 197
QY 172 NWQVEKPDHLFTGLIHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYN 231
Db 198 AMYQRPQSGPKLLIYWASTRSGVPDRFTGSGGTDFTLTISVQAEDLAIYICKQSYT 257
QY 232 NHWVFGGGTKLTVLGQPKSAAGSEOKLISEEDLNSHHHH 272
Db 258 LR-TFGGGTKLEI-----KREQKLISEEDLNHHHHH 288

RESULT 7
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
;   immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948, 004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

Query Match      47.3%; Score 696; DB 2; Length 495;
Best Local Similarity 51.2%; Pred. No. 2.3e-44;
Matches 147; Conservative 29; Mismatches 59; Indels 52; Gaps 7;

QY 2 AOVLQOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 61
Db 246 SDIKLQOQSGAELARPGASVMSCKTSYFTFTYTHWVRQPHDLEWIGYNPSEGYN 305
QY 62 YNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGQTT 121
Db 306 YNQKFKDKATLTADKSSNTAYMQLSLTSEDSAVYICARYD---DHVCLDYWRQGTTL 361
QY 122 TVSSAKTTPKLG-----DIQAVVTQBSA-LTTSPEGTVTLTCSRNTGTV 166
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;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB98/01294
;   FILING DATE: 05-MAY-1998
;   APPLICATION NUMBER: GB 9709421.3
;   FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 38:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 288 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match      46.6%; Score 685; DB 2; Length 258;
Best Local Similarity 56.1%; Pred. No. 7.1e-44;
Matches 147; Conservative 32; Mismatches 59; Indels 24; Gaps 6;

QY 1 MAQVLOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 60
Db 1 MAQVLOQSGAELARPGASVMSCKTSYFTFTSYWNVWVKRPGQGLEWIGINPTGT 60
QY 61 DYNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGQTT 120
Db 61 KYNQFKDKATLTADKSSNTAYMQLSLTINVDNAVYCTT-----GYSYFDYWGQGT 113
QY 121 VTSSAKTTPKLG-----DIQAVVTQBSA-LTTSPEGTVTLTCSRNTGTVTSNYANW 173
Db 114 VTSSGGGGGGGGGGGGGSDIE--LTQSPAIMSASPGKVTITCSASSV----NYMHW 167
QY 174 VQEKPDHLFTGLIHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNH 233
Db 168 FOQKPGTSPKLIWISSTSNLASGVPARFSGSGSGTSYSLTISRMEADAATYYICQQRSSYP 227
QY 234 WYFGGGTKLTVLGQPKSAAGS 255
Db 228 YTFGGGTKL----QIKRAAGA 245

RESULT 9
US-08-279-772A-8
; Sequence 8, Application US/08279772A
; Patent No. 6080560
; GENERAL INFORMATION:
; APPLICANT: Russell, David R
; APPLICANT: Fuller, James T
; TITLE OF INVENTION: Method for Producing Antibodies in Plant
;   Cells
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Quarles and Brady
;   STREET: PO Box 2113
;   CITY: Madison
;   STATE: WI
;   COUNTRY: United States of America
;   ZIP: 53701-2113
```



```

; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-57

Query Match 46.1%; Score 677; DB 1; Length 246;
Best Local Similarity 55.1%; Pred. No. 2.7e-43;
Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

QY 3 QVLOQSGAELARPGASVMSCKASGYFTFTTIHWVRQPGHDLWIGYINPSSGYSY 62
Db 1 QVQLQSGAELVKPGASVMSCKASGYTFASYWINVVKQPGGLEWIGHIYVRSITKY 60
QY 63 NQNFPGKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFYAWGQGTTVT 122
Db 61 NEKFKSKATLTLDTSSTAYMQLSSLTSDSAVYYCSRG---DGSYYAMDYWGQGTTVT 117
QY 123 VSSAKTTPKLGDIQAVVTOESA-LTTSFGETVTLTCRNTGTVTTSNYANWVQKPDHL 181
Db 118 VSSG-----GGSDIELTQSPAILSPGKVTMTCRASSV----SYMHWYQQKPGSS 167
QY 182 FTGLIGHTNNRAGVPAREGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTK 241
Db 168 PKWIVATSNLAGVPTREFSGTSGTSYSLTISRVEADAATYYCQWSENPTFFSGTK 227
QY 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
Db 228 LEI-----KRAAA--EQKLISEEDLN 246

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RESULT 12
US-08-469-658-57
; Sequence 57, Application US/0849658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994

```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-658-57

Query Match 46.1%; Score 677; DB 1; Length 246;
Best Local Similarity 55.1%; Pred. No. 2.7e-43;
Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

QY 3 QVLOQSGAELARPGASVMSCKASGYFTFTTIHWVRQPGHDLWIGYINPSSGYSY 62
Db 1 QVQLQSGAELVKPGASVMSCKASGYTFASYWINVVKQPGGLEWIGHIYVRSITKY 60
QY 63 NQNFPGKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFYAWGQGTTVT 122
Db 61 NEKFKSKATLTLDTSSTAYMQLSSLTSDSAVYYCSRG---DGSYYAMDYWGQGTTVT 117
QY 123 VSSAKTTPKLGDIQAVVTOESA-LTTSFGETVTLTCRNTGTVTTSNYANWVQKPDHL 181
Db 118 VSSG-----GGSDIELTQSPAILSPGKVTMTCRASSV----SYMHWYQQKPGSS 167
QY 182 FTGLIGHTNNRAGVPAREGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTK 241
Db 168 PKWIVATSNLAGVPTREFSGTSGTSYSLTISRVEADAATYYCQWSENPTFFSGTK 227
QY 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
Db 228 LEI-----KRAAA--EQKLISEEDLN 246

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RESULT 13
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Huananus
; US-09-526-738A-2

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Query Match 46.0%; Score 676; DB 2; Length 256;
Best Local Similarity 55.8%; Pred. No. 3.3e-43;
Matches 145; Conservative 32; Mismatches 59; Indels 24; Gaps 6;

QY 3 QVLOQSGAELARPGASVMSCKASGYFTFTTIHWVRQPGHDLWIGYINPSSGYSY 62
Db 1 QVQLQSGAELAKPGASVMSCKTSGYTFSTYMMNVVKQPGGLEWIGYINPTTGYTKY 60
QY 63 NQNFPGKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFYAWGQGTTVT 122
Db 61 NQKFKDKATLTADKSSNTAYMQLSSLTNTVDSAVYYCTT-----GYSYFDYWGQGTTVT 113

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QY 123 VSSAKTTPKLG-----DIOAVVTOESA-LTSPGEBVTLTCSRNTGTVTTNSYANWVQ 175
DB 114 VSSGGGGGGGGGGGGSDIE--LTSPAIMSAPGKVTITCSASSV-----NYMWFQ 167
QY 176 EKPDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTTTGAQTEDEAIFYCALWNNHW 235
DB 168 QKPGTSPKMWISSTNLASGVPARFSGSGTSLTISRMEADAATYCYQORSSVPT 227
QY 236 FGGGKTLTVLGQPKSAAGS 255
DB 228 FGGGTKL-----QIKRAAGA 243

RESULT 14

US-08-463-163-3
; Sequence 3, Application US/08463163
; Patent No. 5696237
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Chaudhary, Vijay K.
; APPLICANT: Pastan, Ira H.
; APPLICANT: Waldmann, Thomas A.
; APPLICANT: Queen, Cary L.
; TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,163
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 06/227,227
; FILING DATE: 22-JAN-1981
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 06/911,227
; FILING DATE: 24-SEP-1986
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,361
; FILING DATE: 21-APR-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,722
; FILING DATE: 08-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-12211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-163-3

Query Match 45.9%; Score 675; DB 1; Length 599;
Best Local Similarity 53.9%; Pred. No. 1.1e-42;
Matches 146; Conservative 31; Mismatches 78; Indels 16; Gaps 4;

QY 3 QVLOQSGAELARPASVMSCKASGYTFTTYTHWVRORPGHDLWIGVINPSSGYSDY 62
DB 2 QVLOQSGAELAKPFGASVMSCKASGYTFTSYRMHWVKORPGQGLEWIGVINPSTGYTEY 61
QY 63 NQNFKKTTLTADKSSNTAYMQLNSLTSDSVAIYCCARRADYCNVEYTWFAVWGQGTVT 122
DB 62 NQKFKDKATLTADKSSSTAYMQLNSLTSDSVAIYCCARRADYCNVEYTWFAVWGQGTTLT 114
QY 123 VSS-----AKTTPKLGSDIOAVVTOESA-LTSPGEBVTLTCSRNTGTVTTNSYANWVQEK 177
DB 115 VSSGGGGGGGGGGGGGQIVLTQSPAIMSAPGKVTITCSAS-----SSISYMHWFQOK 170
QY 178 PDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTTTGAQTEDEAIFYCALWNNHWVFG 237
DB 171 PGTSPLMWIYVTTNLSAGVPARFSGSGTSLTISRMEADAATYCYQORSTYPLTFG 230
QY 238 GGTKLTVLGQPKSAAGSEKLISEEDLNH 268
DB 231 SGTKLKGGSLAALTAHQACHLPLETFTTRH 261

RESULT 15

US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSEW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESCA
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-20

Query Match      44.9%; Score 659.5; DB 1; Length 244;
Best Local Similarity 55.8%; Pred. No. 5.4e-42;
Matches 140; Conservative 33; Mismatches 61; Indels 17; Gaps 7;

QY 3 QVQLQSGAELARPASVMSCKASGYTFYTIHWVRORPGHLEWIGYINPSSGYSY 62
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLQSGAELVPGASVKLCKASGYTFSSHWMHWKQKAGQGLEWIGFNPNGRTNY 60

QY 63 NQPFKKTTLTADKSSNTAYMQLNSLTSDSAVYCCARRADYCNVEYTWFAWQGQTTVT 122
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NEKFKSKATLTVDKSSSTAYMQLSSLTSDSAVYCASR-DY-DYDGRYFDYWQGQTTVT 118

QY 123 VSSAKTTPKLG-----DIQAVVTQESA-LTTPGETVLTCSRNTGTVTSNYANWVQ 175
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 VSFGGGGGGGGGGGSDIE--LTOSPALMSAPGEKVTMTCSASSV-----SYWYVYQ 172

QY 176 EKPDLFTGLIHTNNRPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALW--YNNH 233
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 QKPGSSPRLLIYDTSNLASGVPVRFSGSGGTSYSLTISRMEADAATYYCQWSSYP 232

QY 234 WVEGGGKLTIV 244
Db :|||||:
233 YTFGGGKLEI 243
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Search completed: February 9, 2006, 03:35:35
Job time : 37.2299 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:53:23 ; Search time 127.57 Seconds
(without alignments)
894.155 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQSGAELARPGASV.....GSEQLISEDLNHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	709	48.2	492	4	US-10-682-845-81
2	707	48.1	492	4	US-10-682-845-63
3	707	48.1	492	4	US-10-682-845-73
4	707	48.1	492	4	US-10-682-845-85
5	706	48.0	492	4	US-10-682-845-61
6	705	48.0	492	4	US-10-682-845-71
7	704	47.9	409	4	US-10-362-591-2
8	704	47.9	492	4	US-10-682-845-59
9	704	47.9	492	4	US-10-682-845-75
10	704	47.9	492	4	US-10-682-845-87
11	704	47.9	500	4	US-10-168-809-22
12	703	47.8	492	4	US-10-682-845-83
13	702	47.8	492	4	US-10-682-845-67
14	701	47.7	492	4	US-10-682-845-65
15	701	47.7	492	4	US-10-682-845-79
16	700.5	47.7	243	5	US-10-879-994-10
17	700.5	47.7	243	5	US-10-610-452-10
18	700	47.6	295	4	US-10-406-830-7
19	700	47.6	492	4	US-10-682-845-69
20	699	47.6	492	4	US-10-682-845-77
21	696	47.3	495	3	US-09-948-004-18
22	696	47.3	495	5	US-10-672-932-18
23	686	46.7	260	4	US-10-435-614-20
24	685	46.6	258	4	US-10-247-488-4
25	684	46.5	260	4	US-10-435-614-19
26	683.5	46.5	249	3	US-09-880-748-1838
27	683.5	46.5	249	4	US-10-293-418-1838

28	681	46.3	291	4	US-10-406-830-6	Sequence 6, Appli
29	679.5	46.2	438	4	US-10-244-821-88	Sequence 88, Appl
30	677	46.1	499	5	US-10-805-177-111	Sequence 111, App
31	676.5	46.0	245	3	US-09-880-748-1523	Sequence 1523, Ap
32	676.5	46.0	245	4	US-10-293-418-1523	Sequence 1523, Ap
33	676	46.0	243	5	US-10-566-406-2	Sequence 2, Appli
34	676	46.0	256	4	US-10-247-488-2	Sequence 2, Appli
35	674.5	45.9	524	5	US-10-805-177-113	Sequence 113, App
36	673	45.8	423	4	US/10/013	Sequence 8, Appli
37	673	45.8	423	4	US/10/150	Sequence 8, Appli
38	673	45.8	423	4	US/10/244	Sequence 48, Appli
39	672.5	45.7	657	5	US-10-723-003-48	Sequence 48, Appl
40	672.5	45.7	657	6	US-11-004-639-48	Sequence 48, Appl
41	672	45.7	145	4	US-10-365-123-45	Sequence 45, Appl
42	671	45.6	291	6	US-11-093-103-102	Sequence 102, App
43	670	45.6	243	5	US-10-966-406-45	Sequence 45, Appl
44	669.5	45.5	258	4	US-10-239-656-59	Sequence 59, Appl
45	667	45.4	248	5	US-10-879-994-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-682-845-81
; Sequence 81, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M58 mutant in anti-CD3 part
US-10-682-845-81

Query Match	48.2%	Score	709;	DB	4;	Length	492;
Best Local Similarity	51.9%	Pred. No.	8e-42;				
Matches	149;	Conservative	28;	Mismatches	58;	Indels	52;
Gaps	7;						
Qy	2	AQVQLQSGAELARPGASVKMSCKASGYTFTYTIHWVRPQGHDLWVGINPSSGYSD	61				
Db	243	SDIKLQSGAELARPGASVKMSCKTSGYTFYTHVVRPQGHDLWVGINPSSGYSD	302				
Qy	62	YNQFKKTKTLTADKSNATYMLNSLTSDSAVYVCARRADYGNVEYTFYFAYVGGQTTV	121				
Db	303	YNQFKKTKTLTADKSNATYMLNSLTSDSAVYVCARRADYGNVEYTFYFAYVGGQTTV	358				
Qy	122	TVSSAKTTPKLGK-----DIQAVTQESA-LTSPGETVTLTCSRNTGVT	166				
Db	359	TVSSVE-----GGSGGGGGGGVDDIQ--LTQSPAIMSASPGKVTMTCRASSSV--	409				
Qy	167	TSNYANVQKPDHLFTGLTHTNRPAGVPARGSLIGDKAALTITGAQTEDEAIYFC	226				
Db	410	--SYNNYQKSGTSPKRWIYDTSKVASGVPRFSGSGTSTSLTSSMEADAATYYC	467				
Qy	227	ALVYNNHWFGGKTLVLGQPKSAAAGSEKLISEDLNHHHHH	273				
Db	468	QQMSSNPLTFGAGTKLEL-----KHHHHH	492				

RESULT 2

RESULT 5
US-10-682-845-61
; Sequence 61, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-61

Query Match 48.0%; Score 706; DB 4; Length 492;
Best Local Similarity 51.6%; Pred. No. 1.3e-41;
Matches 148; Conservative 29; Mismatches 58; Indels 52; Gaps 7;

QY 2 AQVOLQOSGAELARPCASVMSCKASGYTFTTTHWVRRPQGHDLIEWIGYNPSSGYSD 61
DB 243 SDIKLQOSGAELARPCASVMSCKTSGYTFTRYTHWVQRPGQGLEWIGYNPSSRGYTN 302
QY 62 YNQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWGGQTTV 121
DB 303 YNQKFKDKATLTITDKSSSTAYMQLSSLTSEDSAVYVCARH----DHYCLDYWGQTTL 358
QY 122 TVSSAKTTPKLG-----DIAQVVTQESA-LTTPSGETVTLTCSRNTGTVT 166
DB 359 TVSSVE-----GGSGGGGGGGVDDIQ--LTQSPAIMSASPGKVTMTCRASSV-- 409
QY 167 TSNYANVQKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAOTDEAIYFC 226
DB 410 --SYMNWYQKSGTSPKRWIYDTSKVASGVPRFSGSGTSYSLTSSMEADAATYTC 467
QY 227 ALWYNNHWVFGGTKLTVLGOPKSAAGSEQKLISEEDLNSHHHH 273
DB 468 QWSSNPLTFGAGTKLEL-----KHHHHH 492

RESULT 6
US-10-682-845-71
; Sequence 71, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M11 mutant in anti-CD3 part
US-10-682-845-71

Query Match 48.0%; Score 705; DB 4; Length 492;
Best Local Similarity 52.3%; Pred. No. 1.5e-41;
Matches 150; Conservative 27; Mismatches 58; Indels 52; Gaps 8;

QY 2 AQVOLQOSGAELARPCASVMSCKASGYTFTTTHWVRRPQGHDLIEWIGYNPSSGYSD 61
DB 243 SDIKLQOSGAELARPCASVMSCKTSGYTFTRYTHWVQRPGQGLEWIGYNPSSRGYTN 302
QY 62 YNQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWGGQTTV 121
DB 303 YNQKFKDKATLTITDKSSSTAYMQLSSLTSEDSAVYVCAR--YFNDHYC-LDYWGQTTL 358
QY 122 TVSSAKTTPKLG-----DIAQVVTQESA-LTTPSGETVTLTCSRNTGTVT 166
DB 359 TVSSVE-----GGSGGGGGGGVDDIQ--LTQSPAIMSASPGKVTMTCRASSV-- 409
QY 167 TSNYANVQKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAOTDEAIYFC 226
DB 410 --SYMNWYQKSGTSPKRWIYDTSKVASGVPRFSGSGTSYSLTSSMEADAATYTC 467
QY 227 ALWYNNHWVFGGTKLTVLGOPKSAAGSEQKLISEEDLNSHHHH 273
DB 468 QWSSNPLTFGAGTKLEL-----KHHHHH 492

RESULT 7
US-10-362-591-2
; Sequence 2, Application US/10362591
; Publication No. US20040072749A1
; GENERAL INFORMATION:
; APPLICANT: ZOCHER, MARCEL
; APPLICANT: BAUERLE, PATRICK
; APPLICANT: DREIER, TORSTEN
; TITLE OF INVENTION: COMPOSITION FOR THE ELIMINATION OF AUTOREACTIVE B-CELLS
; FILE REFERENCE: 029976-0110
; CURRENT APPLICATION NUMBER: US/10/362,591
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09714
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: EP 00117354.1
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-591-2

Query Match 47.9%; Score 704; DB 4; Length 409;
Best Local Similarity 51.6%; Pred. No. 1.5e-41;
Matches 148; Conservative 29; Mismatches 58; Indels 52; Gaps 7;

QY 2 AQVOLQOSGAELARPCASVMSCKASGYTFTTTHWVRRPQGHDLIEWIGYNPSSGYSD 61
DB 160 SDIKLQOSGAELARPCASVMSCKTSGYTFTRYTHWVQRPGQGLEWIGYNPSSRGYTN 219
QY 62 YNQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWGGQTTV 121
DB 220 YNQKFKDKATLTITDKSSSTAYMQLSSLTSEDSAVYVCARYD-----DHYCLDYWGQTTL 275
QY 122 TVSSAKTTPKLG-----DIAQVVTQESA-LTTPSGETVTLTCSRNTGTVT 166
DB 276 TVSSVE-----GGSGGGGGGGVDDIQ--LTQSPAIMSASPGKVTMTCRASSV-- 326
QY 167 TSNYANVQKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAOTDEAIYFC 226
DB 327 --SYMNWYQKSGTSPKRWIYDTSKVASGVPRFSGSGTSYSLTSSMEADAATYTC 384
QY 227 ALWYNNHWVFGGTKLTVLGOPKSAAGSEQKLISEEDLNSHHHH 273
DB 385 QWSSNPLTFGAGTKLEL-----KHHHHH 409

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:55:47 ; Search time 19,9009 Seconds
(without alignments)
180.014 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQQSGAELARPGASV.....GSRQKLISBEDLNHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	683.5	46.5	249	7	US-11-054-515-1838
2	676.5	46.0	245	7	US-11-054-515-1523
3	674	45.9	615	6	US-10-512-184-50
4	668.5	45.5	290	7	US-11-032-773-957
5	660.5	44.9	245	7	US-11-054-515-1919
6	659	44.8	319	7	US-11-032-773-955
7	654	44.5	250	7	US-11-054-515-1722
8	651.5	44.3	247	7	US-11-054-515-948
9	651	44.3	248	7	US-11-054-515-1643
10	651	44.3	250	7	US-11-054-515-1723
11	650.5	44.3	247	7	US-11-054-515-927
12	649	44.1	248	7	US-11-054-515-893
13	647	44.0	248	7	US-11-054-515-1681
14	646.5	44.0	251	7	US-11-054-515-1496
15	646	43.9	254	7	US-11-054-515-2082
16	644.5	43.8	251	7	US-11-054-515-1688
17	644	43.8	248	7	US-11-054-515-1609
18	643.5	43.8	251	7	US-11-054-515-1459
19	643	43.7	248	7	US-11-054-515-1679
20	642.5	43.7	253	7	US-11-054-515-1936
21	640.5	43.6	243	7	US-11-054-515-1959
22	640	43.5	248	7	US-11-054-515-1622
23	639	43.5	248	7	US-11-054-515-1660
24	639	43.5	248	7	US-11-054-515-1670
25	639	43.5	248	7	US-11-054-515-1755

26	638.5	43.4	249	7	US-11-054-515-1753	Sequence 1753, Ap
27	637.5	43.4	249	7	US-11-054-515-1299	Sequence 1299, Ap
28	637.5	43.4	255	7	US-11-054-515-1156	Sequence 1156, Ap
29	637	43.3	248	7	US-11-054-515-950	Sequence 950, App
30	637	43.3	248	7	US-11-054-515-953	Sequence 953, App
31	637	43.3	248	7	US-11-054-515-1181	Sequence 1181, Ap
32	637	43.3	248	7	US-11-054-515-1623	Sequence 1623, Ap
33	636.5	43.3	249	7	US-11-054-515-1290	Sequence 1290, Ap
34	636	43.3	248	7	US-11-054-515-900	Sequence 900, App
35	636	43.3	248	7	US-11-054-515-1293	Sequence 1293, Ap
36	636	43.3	248	7	US-11-054-515-1721	Sequence 1721, Ap
37	636	43.3	248	7	US-11-054-515-1647	Sequence 1647, Ap
38	636	43.3	250	7	US-11-054-515-2031	Sequence 2031, Ap
39	635.5	43.2	241	7	US-11-054-515-1077	Sequence 1077, Ap
40	635.5	43.2	251	7	US-11-054-515-2106	Sequence 2106, Ap
41	635	43.2	242	7	US-11-054-515-1192	Sequence 1192, Ap
42	635	43.2	246	7	US-11-054-515-1462	Sequence 1462, Ap
43	635	43.2	252	7	US-11-054-515-1699	Sequence 1699, Ap
44	635	43.2	254	7	US-11-054-515-1699	Sequence 1699, Ap
45	635	43.2	256	7	US-11-054-515-1621	Sequence 1621, Ap

ALIGNMENTS

RESULT 1

US-11-054-515-1838
; Sequence 1838, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1838

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-1838

Query Match 46.5%; Score 683.5; DB 7; Length 249;

Best Local Similarity 55.6%; Pred. No. 2.7e-37;

Matches 139; Conservative 32; Mismatches 72; Indels 7; Gaps 3;

Qy 3 QVQLQQSGAELARPGASVQMSCKASGYTFYTHWVRQRPGHDLIEWIGINPSSGSDY 62

Db 1 QVQLQQSGAEVTKGSSVKVSKASGGTFNNFASWRQAFQGLWVGGITPLFGTNY 60

Qy 63 QNPFKGTTLTPADKSSNTAYMQLNSLTSEDASVYCCARRADYNNYETWFAYWGQGTVT 122

Db 61 AERLQGRVTTITADELRTVTVMELSSLRSEDTAVVYCARESEGGDYTNP-FGYWGRGTTVT 119
Qy 123 VS-----SAKTPKLGDDIOAVVTOESALTTSPGETVTLTCRNTGTVTTSYANVWQEK 177
Db 120 VSSGGGGSGGGSGGSAQAVVIOBPSLTVSPGTVTLTCTSTGAVTNNNYPSWFOOK 179
Qy 178 PDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAOTDEAIYFCALWYNN-HWVF 236
Db 180 PGQAPRLISWNNRSPWTPARFSAVLLGGKAVLTLSGVQPEDEABEYICLLYSGDAQLVF 239
Qy 237 GGGTKLTVLG 246
Db 240 GGGKTVLG 249

RESULT 2

US-11-054-515-1523
; Sequence 1523, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1523
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1523

Query Match 46.0%; Score 676.5; DB 7; Length 245;
Best Local Similarity 56.8%; Pred. No. 7.3e-37;
Matches 142; Conservative 27; Mismatches 69; Indels 13; Gaps 4;
Qy 3 QVLOQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLWIGYINPSSGYSY 62
Db 1 QVQLVSGAEVKPGSVKVKCKASGTVSSRIISNVRQAPGQGLEWMGSLPSPGAPYI 60
Qy 63 NQMFKGTTLTADKSNNTAYMQLNSLTSEDSAVVYCARRADYGNVYTWFAVWGQTTVT 122
Db 61 AQFQGRVAITDALNTAFMELRSKSDDTAVVYCAR--DQGRY----LDLWKGKTLVT 114
Qy 123 VS-----SAKTPKLGDDIOAVVTOESALTTSPGETVTLTCRNTGTVTTSYANVWQEK 177
Db 115 VSSGGGGSGGGSGGSAQAVVIOBPSLTVSPGTVTLTCSITGAVTSGNTPNPFQOK 174
Qy 178 PDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAOTDEAIYFCALWYNN--NHWV 235
Db 175 PGQAPRALIYSTDNKHSWTPARFSGSLIGDKAALTLSGVQPEDEADYICLLYGGAPWV 234

Qy 236 FGGGTKLTVLG 246
Db 235 FGGGKTVTVLG 245

RESULT 3

US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv SS2 - cmvC/His6.
US-10-512-184-50

Query Match 45.9%; Score 674; DB 6; Length 615;
Best Local Similarity 51.9%; Pred. No. 2.3e-36;
Matches 148; Conservative 33; Mismatches 80; Indels 24; Gaps 8;
Qy 1 MAQVQLQQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLWIGYINPSSGYS 60
Db 342 MAQVQLQQSGTVLARPGASVKMSCKASGYTFYTHHWVRQPGQGLEWIGAIYPCGNSDT 401
Qy 61 DYNQMFKGTTLTADKSNNTAYMQLNSLTSEDSAVVYCARRADYGNVYTWFAVWGQTT 120
Db 402 SYNQKPKRAKLTAVTSTAYMELSSLTNEBSAVVYCTR---DWDYA-MDYWGQGYTS 456
Qy 121 VTVSSAKTT-----PKLG---GDIQAVVTQESA-LTTSPTGETVTLTCRNTGTVTTSNY 170
Db 457 VTVSSGTSVSGSKPGEGESTKGADIVLFQSPVMSASPGKVTWTCASSSV----NY 512
Qy 171 ANNVQEKPDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAOTDEAIYFCALWY 230
Db 513 IVVYQWKSGTSPKRWIFDTSKLASGVVRFSGSGSGTSPSLTSSMEADIATYYCQQWS 572
Qy 231 NNHWVFGGTKLTVLGQPKSAAGSEOKLISEDLNS--HHHHH 273
Db 573 SPPLTFGAGTKLEL---KRAVDAAAFQKLISEDLGALDHHHHH 614

RESULT 4

US-11-032-773-957
; Sequence 957, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 290


```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD S1C5 V5 His protein sequence
US-11-032-773-957

Query Match          45.5%; Score 668.5; DB 7; Length 290;
Best Local Similarity 50.0%; Pred. No. 2.7e-36;
Matches 147; Conservative 38; Mismatches 84; Indels 25; Gaps 7;

Qy 1 MAQVQLQSGAEELARPGASVMSCKASGYTFYTHHWVRQPGHDLIEWIGYINPSSGYS 60
Db 1 MAEVQLQSGAEELVKGASVKVSKASGYTFSTYMHVWRQPGGLEWIGIINPSSGSTSY 60

Qy 61 DYNQFKGKTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVETWPAWQGGTT 120
Db 1 MAEVQLQSGAEELVKGASVKIISKASGYTFDTHVHWVRQPGGLEWIGFISPGNGDI 60

Qy 61 RYNEKFKDKATLTADKSSNTAYMQLNSLTSEDSAVYFCRKSFY--YDNYGDMWQGGTT 118
Db 1 RYNEKFKDKATLTADKSSNTAYMQLNSLTSEDSAVYFCRKSFY--YDNYGDMWQGGTT 118

Qy 121 VTSSAKTT-----PKLGGDIQAVVTQESA-LTTSFGETVTLTCSRNTGVTVTSNYA 171
Db 119 LTVSSSGAPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176

Qy 172 NWVQKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTTITCAQTEDEAIYFCALWYN 231
Db 177 HWYQKPGSPKLIWYTTSLAGVPARFSGSGGTSYSLTISMEAEADAATYCHQYHR 236

Qy 232 NHWVFGGKTKLTVL---GQPKSAAGS-----EQKLISEEDLN---HHHHH 273
Db 237 SPLTFGAGTKLELKRAADAAPTVAASAFKLPINLLGLDSTNSAVDHHHHH 290
```

```
RESULT 5
US-11-054-515-1919
; Sequence 1919, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1919
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1919

Query Match          44.9%; Score 660.5; DB 7; Length 245;
Best Local Similarity 54.5%; Pred. No. 7.6e-36;
Matches 138; Conservative 34; Mismatches 64; Indels 17; Gaps 5;
```

```
Qy 3 QVQLQSGAEELARPGASVMSCKASGYTFYTHHWVRQPGHDLIEWIGYINPSSGYS 62
Db 1 EVQLVQSGAEVVKPGASVKVSKASGYTFSTYMHVWRQPGGLEWIGIINPSSGSTSY 60

Qy 63 NQNFQKGTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVETWPAWQGGTT 122
Db 61 AQFGQGVMTWTRDTSTVYMLSSLRSEDATVYVCARDLS-GSYFSRYFDYWGQGLT 119

Qy 123 VSS---AKTTPKLGSDIQAVVTQESALTTSPGETVTLTCSRNTGVTVTSNYANWVQKPD 179
Db 120 VSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176

Qy 180 HLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTTITCAQTEDEAIYFCALWYN-----NH 233
Db 177 QAPVLVIYKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYC----NSRDSGNH 232

Qy 234 WYFGGKTKLTVLG 246
Db 233 WYFGGKTKLTVLG 245

RESULT 6
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD S1C5 CD20 His Protein Sequence
US-11-032-773-955

Query Match          44.8%; Score 659; DB 7; Length 319;
Best Local Similarity 45.8%; Pred. No. 1.2e-35;
Matches 148; Conservative 38; Mismatches 83; Indels 54; Gaps 7;
```

```
Qy 1 MAQVQLQSGAEELARPGASVMSCKASGYTFYTHHWVRQPGHDLIEWIGYINPSSGYS 60
Db 1 MAEVQLQSGAEELVKGASVKIISKASGYTFDTHVHWVRQPGGLEWIGFISPGNGDI 60

Qy 61 DYNQFKGKTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVETWPAWQGGTT 120
Db 61 RYNEKFKDKATLTADKSSNTAYMQLNSLTSEDSAVYFCRKSFY--YDNYGDMWQGGTT 118

Qy 121 VTSSAKTT-----PKLGGDIQAVVTQESA-LTTSFGETVTLTCSRNTGVTVTSNYA 171
Db 119 LTVSSSGAPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176

Qy 172 NWVQKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTTITGAQTEDEAIYFCALWYN 231
Db 177 HWYQKPGSPKLIWYTTSLAGVPARFSGSGGTSYSLTISMEAEADAATYCHQYHR 236

Qy 232 NHWVFGGKTKLTVL---GQPKSAAGS-----EQKLISEEDLN---HHHHH 273
Db 237 SPLTFGAGTKLELKRAADAAPTVAASAFKLPINLLGLDSTNSAVDHHHHH 290

Qy 267 -----SHHHHH 273
Db 297 SEKNPSTQYCNASVDHHHHH 319
```

```
RESULT 7
US-11-054-515-1722
; Sequence 1722, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1722
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (227)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-1722

Query Match 44.5%; Score 654; DB 7; Length 250;
Best Local Similarity 53.3%; Pred. No. 2e-35;
Matches 137; Conservative 35; Mismatches 65; Indels 20; Gaps 5;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRPGHDLHWIGYINPSSGYSDY 62
DB 1 QVQLQSGAEVKPKGASVKVSKASGYTFYTHHWVRQAPGQGLEWMGMINENSGGTNY 60
QY 63 NQNFKGKTLTADKSNATAYMOLNSLTSEDSAVVYCARADY----GNYEYTFAYWGQ 118
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSDDTAVYCARVLPHYDILTGYSONWFDPMGRG 120
QY 119 TTVTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWQ 175
DB 121 TLTVSSGGGGSGGGSGGSSSELQDPAVSVLQGTVRITCQ---GDSLRSYVYASWQ 177
QY 176 EKPDHLFTGLHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYN---- 231
DB 178 QKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC-----NSRDS 233
QY 232 --NHVFGGKTLTVLG 246
DB 234 SGNHVFGGKTLTVLG 250

RESULT 8
US-11-054-515-948
; Sequence 948, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
```

```
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 948
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (227)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-948

Query Match 44.3%; Score 651.5; DB 7; Length 247;
Best Local Similarity 54.3%; Pred. No. 2.8e-35;
Matches 138; Conservative 34; Mismatches 65; Indels 17; Gaps 5;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRPGHDLHWIGYINPSSGYSDY 62
DB 1 QVQLVQSGAEVKPKGASVKVSKASGYTFYTHHWVRQAPGQGLEWMGMNPNSTGY 60
QY 63 NQNFKGKTLTADKSNATAYMOLNSLTSEDSAVVYCARADYGNV----EYTFAYWGQ 117
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSDDTAVYCAR---GQYDILTGYNWFDPWGX 116
QY 118 GTTVTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWV 174
DB 117 GTLTVSSGGGGSGGGSGGSSSELQDPAVSVLQGTVRITCQ---GDSLRSYVYASWY 173
QY 175 QKPDHLFTGLHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCAL--WYNN 232
DB 174 QKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNXRDSGN 233
QY 233 HHVFGGKTLTVLG 246
DB 234 HHVFGGKTLTVLG 247

RESULT 9
US-11-054-515-1643
; Sequence 1643, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
```



```
Qy 177 KPDHLFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYN----- 231
Db 177 KPGQAPVLVIYGNRPSGIPDRFSGSSGNTASLITGAQAEADYYC-----NSRDS 232

Qy 232 -NHWFVGGGKTLTVLG 246
Db 233 GNHWFVGGGKTLTVLG 248

RESULT 14
US-11-054-515-1496
; Sequence 1496, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1496
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1496

Query Match 44.0%; Score 646.5; DB 7; Length 251;
Best Local Similarity 52.8%; Pred. No. 6e-35;
Matches 133; Conservative 40; Mismatches 70; Indels 9; Gaps 5;

Qy 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHHWVRQRPQGHDLWIGYINPSSGYSY 62
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYSTFTHHWVRQAPGQRLRWGMINVGNTKY 60

Qy 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVVYCARADYGYE-YTNF-AVWGQGT 120
Db 61 SQKLQGRVITRDISASTAYMELSLRSEDFAVYICA-RSDYDILTGYWPAVWGQGT 119

Qy 121 VTVS-----SAKTTPKLGGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSYANWVQ 175
Db 120 VTVSSGGGGGGGGGGGSAQSVLTQPPSAGSPGQSVTISCTGGSSDVGGYNYVYQ 179

Qy 176 EKPDLHFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWY--NNHW 234
Db 180 QYPGKAPKLIYNEVKNRPSGVPDRFSGSKSGNTASLTVSGLQAEDEANYCASYAGNNV 239

Qy 235 VFGGKTLTVLG 246
Db 240 VFGGKTLTVLG 251

RESULT 15
```

```
US-11-054-515-2082
; Sequence 2082, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2082
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2082

Query Match 43.9%; Score 646; DB 7; Length 254;
Best Local Similarity 51.6%; Pred. No. 6.5e-35;
Matches 131; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHHWVRQRPQGHDLWIGYINPSSGYSY 62
Db 1 QVQLVQSGADVKKPGASVRVSKASGYTTSYTHHWVRQAPGRLRWGMINPSSGATNY 60

Qy 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVVYCARADYGYE---YTNFAYWGQGT 119
Db 61 AQPFQGRVITRDTSTTVTMELSSLRFEDTAIYICVRDADEGLVEAETTNWFDWGQGT 120

Qy 120 TVTVS-----SAKTTPKLGGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSYANWV 174
Db 121 MVTVSSGGGGGGGGGGGSAQSVLTQPPSVSGAPQSVTISCTGGSSNIGASVDVNWY 180

Qy 175 QEPDHLFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWY--N 232
Db 181 QQLPGTAPKLLISGNTNRPSGVPDRFSGNSGTSASLAITGLQAEADYYCQSYDLS 240

Qy 233 HWVFGGKTLTVLG 246
Db 241 GWVFGGKTLTVLG 254

Search completed: February 9, 2006, 04:00:32
Job time : 20.9009 secs
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